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OM protein - protein search, using sw model

Run on: February 24, 2006, 08:55:09 ; Search time 18 Seconds
(without alignments)
291.129 Million cell updates/sec

Title: US-09-978-360A-437

Perfect score: 1831

Sequence: 1 MESGRPSLCPILGTTSV.....PKKPCRCQALTRVPLVNS 352

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 117670 seqs, 14887254 residues

Total number of hits satisfying chosen parameters: 117670

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA New:*

1: /cgn2_6/ptodata/2/pubppa/US08_NEW_PUB.pep.*
2: /cgn2_6/ptodata/2/pubppa/US06_NEW_PUB.pep.*
3: /cgn2_6/ptodata/2/pubppa/US07_NEW_PUB.pep.*
4: /cgn2_6/ptodata/2/pubppa/PCT_NEW_PUB.pep.*
5: /cgn2_6/ptodata/2/pubppa/US09_NEW_PUB.pep.*
6: /cgn2_6/ptodata/2/pubppa/US10_NEW_PUB.pep.*
7: /cgn2_6/ptodata/2/pubppa/US11_NEW_PUB.pep.*
8: /cgn2_6/ptodata/2/pubppa/US60_NEW_PUB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result- No.	Score	Match	Query Length	DB ID	Description
1	1831	100.0	352	US-09-978-360A-437	Sequence 437, App
2	155.5	8.5	723	US-11-072-512-2572	Sequence 2572, App
3	143.5	7.8	363	US-11-072-512-3425	Sequence 3425, App
4	112	6.1	795	US-11-072-512-2378	Sequence 2378, App
5	107	5.8	593	US-11-169-041-239	Sequence 239, App
6	107	5.8	619	US-11-072-512-2497	Sequence 2497, App
7	99	5.4	843	US-11-072-512-2043	Sequence 2043, App
8	98.5	5.4	149	US-11-226-657-205	Sequence 205, App
9	98.5	5.4	166	US-11-226-657-204	Sequence 204, App
10	98.5	5.4	355	US-11-135-855-44	Sequence 44, App
11	98.5	5.4	491	US-11-069-642-137	Sequence 137, App
12	98	5.4	203	US-11-024-959-509	Sequence 509, App
13	97	5.3	574	US-10-821-234-164	Sequence 164, App
14	95.5	5.2	645	US-11-072-512-2588	Sequence 2588, App
15	93.5	5.1	670	US-11-072-512-2035	Sequence 2035, App
16	93	5.1	381	US-09-978-360A-712	Sequence 712, App
17	92	5.0	916	US-10-467-657-4242	Sequence 4242, App
18	90	4.9	610	US-11-072-512-2672	Sequence 2672, App
19	89.5	4.9	328	US-11-024-959-517	Sequence 517, App
20	89.5	4.9	2036	US-11-072-512-3564	Sequence 3564, App
21	89	4.9	2036	US-11-124-368A-276	Sequence 276, App
22	89	4.9	2036	US-11-124-368A-280	Sequence 280, App
23	89	4.9	2036	US-11-124-368A-281	Sequence 281, App
24	89	4.9	2044	US-11-124-368A-278	Sequence 278, App
25	89	4.9	2144	US-11-124-368A-277	Sequence 277, App

ALIGNMENTS

26	87	4.8	664	7	US-11-124-367A-439	Sequence 439, App
27	87	4.8	667	7	US-11-124-367A-440	Sequence 440, App
28	86	4.7	360	6	US-10-834-397-293	Sequence 293, App
29	86	4.7	360	7	US-11-165-067A-26	Sequence 26, App
30	85.5	4.7	262	7	US-11-072-512-2104	Sequence 2104, App
31	83.5	4.6	451	7	US-11-054-168B-6	Sequence 6, App
32	83	4.5	381	6	US-10-517-919-326	Sequence 326, App
33	82.5	4.5	306	7	US-11-074-176-290	Sequence 290, App
34	82.5	4.5	421	7	US-11-098-686-10798	Sequence 10798, App
35	82.5	4.5	2630	7	US-11-186-731-2	Sequence 2, App
36	82.5	4.5	7968	7	US-11-186-731-5	Sequence 5, App
37	81.5	4.5	648	6	US-10-793-626-568	Sequence 568, App
38	81.5	4.5	4384	6	US-10-821-234-1120	Sequence 1120, App
39	81	4.4	1165	7	US-11-197-380-6	Sequence 6, App
40	81	4.4	1482	7	US-11-181-330-2	Sequence 2, App
41	80.5	4.4	430	7	US-11-098-686-11038	Sequence 11038, App
42	80.5	4.4	471	7	US-11-072-512-3482	Sequence 3482, App
43	80.5	4.4	547	6	US-10-177-412-2	Sequence 2, App
44	80.5	4.4	816	7	US-11-072-512-2341	Sequence 2341, App
45	80.5	4.4	8746	7	US-11-098-686-10232	Sequence 10232, App

RESULT 1
US-09-978-360A-437
Sequence 437, Application US/09978360A
GENERAL INFORMATION:
Publication No. US2006009633A9
APPLICANT: Edwards, Jean-Baptiste Dumas Milne
APPLICANT: Duchet, Aymeric
APPLICANT: Bouguet, Lydie
APPLICANT: Jobert, Severin
APPLICANT: Clusel, Catherine
TITLE OF INVENTION: Complementary DNA's Encoding Proteins with Signal Peptides
FILE REFERENCE: 56 US4, CIP
CURRENT APPLICATION NUMBER: US/09/978,360A
CURRENT FILING DATE: 2001-10-15
PRIOR APPLICATION NUMBER: US 60/066,677
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: US 60/069,957
PRIOR FILING DATE: 1997-12-17
PRIOR APPLICATION NUMBER: US 60/074,121
PRIOR FILING DATE: 1998-02-09
PRIOR APPLICATION NUMBER: US 60/081,563
PRIOR FILING DATE: 1998-04-13
PRIOR APPLICATION NUMBER: US 60/096,116
PRIOR FILING DATE: 1998-08-10
PRIOR APPLICATION NUMBER: US 60/099,273
PRIOR FILING DATE: -09-04
PRIOR APPLICATION NUMBER: US 09/191,997
PRIOR FILING DATE: 1998-11-13
PRIOR APPLICATION NUMBER: US 09/215,435
PRIOR FILING DATE: 1998-12-17
PRIOR APPLICATION NUMBER: PCT/IB98/02122
PRIOR FILING DATE: 1998-12-17
PRIOR APPLICATION NUMBER: US 09/247,155
PRIOR FILING DATE: 1999-02-09
Remaining Prior Application data removed - See file Wrapper or PALM.
NUMBER OF SEQ ID NOS: 810
SOFTWARE: Patent.pm
SEQ ID NO 437
LENGTH: 352
TYPE: PRT
ORGANISM: Homo Sapiens
FEATURE:
NAME/KEY: SIGNAL
LOCATION: -23..-1
US-09-978-360A-437
Query Match 100.0%; Score 1831; DB 5; Length 352;
Best Local Similarity 100.0%; Pred. No. 2.4e-154;

Matches 352; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MESGGRBPLCOFILIGTTSVTTAALYSYTRQKARVSOELKAKKVLHGEDLKSILSBAPG 60
 Db 1 MESGGRBPLCOFILIGTTSVTTAALYSYTRQKARVSOELKAKKVLHGEDLKSILSBAPG 60

QY 61 KCVPAVAVEGAVRSVKETLINSQFVENCCKVIOQLTLQEHKMMVNRTHLWMDCKSLIHOR 120
 Db 61 KCVPAVAVEGAVRSVKETLINSQFVENCCKVIOQLTLQEHKMMVNRTHLWMDCKSLIHOR 120

QY 121 TMTVPFDLVPHEDGDVAVARVLKPLDSVDLGLFTVYKFKHPSISQFTDVI GHYISGERPK 180
 Db 121 TMTVPFDLVPHEDGDVAVARVLKPLDSVDLGLFTVYKFKHPSISQFTDVI GHYISGERPK 180

QY 181 GIOETEBELKVGAITLTGGLVLDNNSVRLQPPKQMOYILSSODPDSLLQROESSVRLW 240
 Db 181 GIOETEBELKVGAITLTGGLVLDNNSVRLQPPKQMOYILSSODPDSLLQROESSVRLW 240

QY 241 KVALVFGFATCATLFFILRKQYLQROERLRLKQMOEFQEHQAQLLSRAKPEDRESLSK 300
 Db 241 KVALVFGFATCATLFFILRKQYLQROERLRLKQMOEFQEHQAQLLSRAKPEDRESLSK 300

QY 301 ACVVCSSFKSCVFLBEGHVCSTECYRALPEPKKPCICQOATRVIPLYNS 352
 Db 301 ACVVCSSFKSCVFLBEGHVCSTECYRALPEPKKPCICQOATRVIPLYNS 352

RESULT 2

US-11-072-512-2572

/ Sequence 2572, Application US/11072512
 / Publication No. US20060029945A1
 / GENERAL INFORMATION:
 / APPLICANT: ISOGAI, TAKAO
 / APPLICANT: SUGIYAMA, TOMOYASU
 / APPLICANT: OTSUKI, TETSUJI
 / APPLICANT: WAKAMATSU, AI
 / APPLICANT: SATO, HIROYUKI
 / APPLICANT: ISHII, SHIZUKO
 / APPLICANT: YAMAMOTO, JUN-ICHI
 / APPLICANT: ISONO, YUUKO
 / APPLICANT: HIO, YURI
 / APPLICANT: OTSUKA, KAORU
 / APPLICANT: NAGAI, KEIICHI
 / APPLICANT: IRIE, RYOTARO
 / APPLICANT: TAMECHIKA, ICHIRO
 / APPLICANT: SEKI, NAOHITO
 / APPLICANT: YOSHIKAWA, TSUTOMU
 / APPLICANT: OTSUKA, MOTOKYUKI
 / APPLICANT: NAGAHARI, KENJI
 / APPLICANT: MASUHO, YASUHIKO
 / TITLE OF INVENTION: Novel full length cDNA
 / FILE REFERENCE: 084335-0191
 / CURRENT APPLICATION NUMBER: US/11/072,512
 / PRIOR FILING DATE: 2005-03-07
 / PRIOR APPLICATION NUMBER: US 60/350,978
 / PRIOR FILING DATE: 2002-01-25
 / PRIOR APPLICATION NUMBER: JP 2001-379298
 / PRIOR FILING DATE: 2001-11-05
 / NUMBER OF SEQ ID NOS: 4096
 / SOFTWARE: PatentIn Ver. 2.1
 / SEQ ID NO 2572
 / LENGTH: 723
 / TYPE: PRT
 / ORGANISM: Homo sapiens
 / US-11-072-512-2572

Query Match

8.5%; Score 155.5; DB 7; Length 723;
 Best Local Similarity 34.3%; Pred. No. 8.5e-06;
 Matches 37; Conservative 16; Mismatches 38; Indels 17; Gaps 3;

QY 259 LRQOYLQORQERILRKQMOEF-----QEHQAQLLSRAKPEDRESLSKACV 304
 Db 618 LRHEILRRVQELDARIQBELKPPMGGEVVTPTAPQEPESVRSPAPELLEVAQSECV 677

QY 305 CLSSFKSCVFLBEGHVCSTECYRALPEPKKPCICQOATRVIPLYNS 352
 Db 678 CLSRAQWLFINGHVCCECCQCCQPL---RTPELCKRODLAQRLRIYHS 722

RESULT 3

US-11-072-512-3425

/ Sequence 3425, Application US/11072512
 / Publication No. US20060029945A1
 / GENERAL INFORMATION:
 / APPLICANT: ISOGAI, TAKAO
 / APPLICANT: SUGIYAMA, TOMOYASU
 / APPLICANT: OTSUKI, TETSUJI
 / APPLICANT: WAKAMATSU, AI
 / APPLICANT: SATO, HIROYUKI
 / APPLICANT: ISHII, SHIZUKO
 / APPLICANT: YAMAMOTO, JUN-ICHI
 / APPLICANT: ISONO, YUUKO
 / APPLICANT: HIO, YURI
 / APPLICANT: OTSUKA, KAORU
 / APPLICANT: NAGAI, KEIICHI
 / APPLICANT: IRIE, RYOTARO
 / APPLICANT: TAMECHIKA, ICHIRO
 / APPLICANT: SEKI, NAOHITO
 / APPLICANT: YOSHIKAWA, TSUTOMU
 / APPLICANT: OTSUKA, MOTOKYUKI
 / APPLICANT: NAGAHARI, KENJI
 / APPLICANT: MASUHO, YASUHIKO
 / TITLE OF INVENTION: Novel full length cDNA
 / FILE REFERENCE: 084335-0191
 / CURRENT APPLICATION NUMBER: US/11/072,512
 / PRIOR FILING DATE: 2005-03-07
 / PRIOR APPLICATION NUMBER: US 60/350,978
 / PRIOR FILING DATE: 2002-01-25
 / PRIOR APPLICATION NUMBER: JP 2001-379298
 / PRIOR FILING DATE: 2001-11-05
 / NUMBER OF SEQ ID NOS: 4096
 / SOFTWARE: PatentIn Ver. 2.1
 / SEQ ID NO 3425
 / LENGTH: 363
 / TYPE: PRT
 / ORGANISM: Homo sapiens
 / US-11-072-512-3425

Query Match

7.8%; Score 143.5; DB 7; Length 363;
 Best Local Similarity 30.1%; Pred. No. 3.6e-05;
 Matches 41; Conservative 28; Mismatches 40; Indels 27; Gaps 7;

QY 224 QDFDILLQROESSVRLWVLAALVF-GFATCATLFFILRKQYLQROERLRLKQMOEFQ 281
 Db 248 EDIBGLTVRQ-----LKEILLRNFVNYKGCCKEKLW-----EKVTRLYKQKGLQ 293

QY 282 HBAQLLSRAKPEDRESLSKA-----CVVCSSFKSCVFLBEGHVCSTECYRALPEPKK 336
 Db 294 --HLVSGAEDONGAVSGGLENLCKICMDSPIDCVLLEGGHNVTCCKCKRNN---C 347

QY 337 PICRQATRVIPLYNS 352
 Db 348 PICRQYIRAVHVERS 363

RESULT 4

US-11-072-512-2378

/ Sequence 2378, Application US/11072512
 / Publication No. US20060029945A1
 / GENERAL INFORMATION:
 / APPLICANT: ISOGAI, TAKAO
 / APPLICANT: SUGIYAMA, TOMOYASU
 / APPLICANT: OTSUKI, TETSUJI
 / APPLICANT: WAKAMATSU, AI
 / APPLICANT: SATO, HIROYUKI
 / APPLICANT: ISHII, SHIZUKO

APPLICANT: YAMAMOTO, JUN-ICHI
APPLICANT: ISONO, YUUKO
APPLICANT: HIO, YURI
APPLICANT: OTSUKA, KAORU
APPLICANT: NAGAI, KEIICHI
APPLICANT: IRIE, RYOTARO
APPLICANT: TAMECHIKA, ICHIRO
APPLICANT: SEKI, NAOHICO
APPLICANT: YOSHIKAWA, TSUTOMU
APPLICANT: OTSUKA, MOTOTYUKI
APPLICANT: NAGAHARI, KENJI
APPLICANT: MASUHO, YASUHIKO
TITLE OF INVENTION: Novel full length cDNA
FILE REFERENCE: 084335-0191
CURRENT APPLICATION NUMBER: US/11/072,512
CURRENT FILING DATE: 2005-03-07
PRIOR APPLICATION NUMBER: US 60/350,978
PRIOR FILING DATE: 2002-01-25
PRIOR APPLICATION NUMBER: JP 2001-379298
PRIOR FILING DATE: 2001-11-05
NUMBER OF SEQ ID NOS: 4096
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2378
LENGTH: 795
TYPE: PRT
ORGANISM: Homo sapiens
US-11-072-512-2378

Query Match 6.1%; Score 112; DB 7; Length 795;
Best Local Similarity 35.9%; Pred. No. 0.068;
Matches 23; Conservative 9; Mismatches 22; Indels 10; Gaps 2;

Qy 285 QLSAKPEDRESLKSACVCLSSFKSCVFLGCGVSCCTECYRALPEPKKCPICRQAIT 344
Db 645 QVSRTKTE-----CVCSDKKAVALFPCGHACACENCANIM---KKCVQCRAYVE 694

Qy 345 RVIP 348
Db 695 RRVF 698

RESULT 5
US-11-169-041-239
Sequence 239, Application US/11169041
Publication No. US20060019284A1
GENERAL INFORMATION:
APPLICANT: Bristol-Myers Squibb Company
TITLE OF INVENTION: IDENTIFICATION OF POLYNUCLEOTIDES FOR PREDICTING ACTIVITY OF
TITLE OF INVENTION: COMPOUNDS THAT INTERACT WITH AND/OR MODULATE PROTEIN TYROSINE
TITLE OF INVENTION: KINASES AND/OR PROTEIN TYROSINE KINASE PATHWAYS IN LUNG CANCER
TITLE OF INVENTION: CELLS
FILE REFERENCE: 10001 NP
CURRENT APPLICATION NUMBER: US/11/169,041
CURRENT FILING DATE: 2005-06-28
PRIOR APPLICATION NUMBER: 60/584,405
PRIOR FILING DATE: 2004-06-30
NUMBER OF SEQ ID NOS: 527
SOFTWARE: PatentIn version 3.2
SEQ ID NO 239
LENGTH: 593
TYPE: PRT
ORGANISM: Homo sapiens
US-11-169-041-239

Query Match 5.8%; Score 107; DB 7; Length 593;
Best Local Similarity 46.0%; Pred. No. 0.12;
Matches 23; Conservative 4; Mismatches 21; Indels 2; Gaps 2;

Qy 293 EDRSLKSA-CVCLSSFKSCVFLGCGVSCCTECYRALPEPKKCPICR 340
Db 181 EDEVSDNSAEVCVCLSDVDTLLPCRHLCNTCADTLRYQANNCPICR 230

RESULT 6
US-11-072-512-2497

Sequence 2497, Application US/11072512
Publication No. US20060029945A1

GENERAL INFORMATION:

APPLICANT: ISOGAI, TAKAO

APPLICANT: SUGIYAMA, TOMOYASU

APPLICANT: OTSUKI, TETSUJI

APPLICANT: WAKAMATSU, AI

APPLICANT: SATO, HIROYUKI

APPLICANT: ISHII, SHIZUKO

APPLICANT: YAMAMOTO, JUN-ICHI

APPLICANT: ISONO, YUUKO

APPLICANT: HIO, YURI

APPLICANT: OTSUKA, KAORU

APPLICANT: NAGAI, KEIICHI

APPLICANT: IRIE, RYOTARO

APPLICANT: TAMECHIKA, ICHIRO

APPLICANT: SEKI, NAOHICO

APPLICANT: YOSHIKAWA, TSUTOMU

APPLICANT: OTSUKA, MOTOTYUKI

APPLICANT: NAGAHARI, KENJI

APPLICANT: MASUHO, YASUHIKO

TITLE OF INVENTION: Novel full length cDNA
FILE REFERENCE: 084335-0191
CURRENT APPLICATION NUMBER: US/11/072,512
CURRENT FILING DATE: 2005-03-07
PRIOR APPLICATION NUMBER: US 60/350,978
PRIOR FILING DATE: 2002-01-25
PRIOR APPLICATION NUMBER: JP 2001-379298
PRIOR FILING DATE: 2001-11-05
NUMBER OF SEQ ID NOS: 4096
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2497
LENGTH: 619
TYPE: PRT
ORGANISM: Homo sapiens
US-11-072-512-2497

Query Match 5.8%; Score 107; DB 7; Length 619;
Best Local Similarity 46.0%; Pred. No. 0.13;
Matches 23; Conservative 4; Mismatches 21; Indels 2; Gaps 2;

Qy 293 EDRSLKSA-CVCLSSFKSCVFLGCGVSCCTECYRALPEPKKCPICR 340
Db 229 EDEVSDNSAEVCVCLSDVDTLLPCRHLCNTCADTLRYQANNCPICR 278

RESULT 7

US-11-072-512-2043

Sequence 2043, Application US/11072512

Publication No. US20060029945A1

GENERAL INFORMATION:

APPLICANT: ISOGAI, TAKAO

APPLICANT: SUGIYAMA, TOMOYASU

APPLICANT: OTSUKI, TETSUJI

APPLICANT: WAKAMATSU, AI

APPLICANT: SATO, HIROYUKI

APPLICANT: ISHII, SHIZUKO

APPLICANT: YAMAMOTO, JUN-ICHI

APPLICANT: ISONO, YUUKO

APPLICANT: HIO, YURI

APPLICANT: OTSUKA, KAORU

APPLICANT: NAGAI, KEIICHI

APPLICANT: IRIE, RYOTARO

APPLICANT: TAMECHIKA, ICHIRO

APPLICANT: SEKI, NAOHICO

APPLICANT: YOSHIKAWA, TSUTOMU

APPLICANT: OTSUKA, MOTOTYUKI

APPLICANT: NAGAHARI, KENJI

APPLICANT: MASUHO, YASUHIKO

TITLE OF INVENTION: Novel full length cDNA
FILE REFERENCE: 084335-0191

RESULT 10
US-11-135-855-44
; Sequence 44, Application US/11135855
; Publication No. US2005025557A1
; GENERAL INFORMATION:
; APPLICANT: SMITHKLINE BEECHAM CORPORATION
; APPLICANT: SMITHKLINE BEECHAM P.L.C.
; TITLE OF INVENTION: NOVEL COMPOUNDS
; FILE REFERENCE: GP50013
; CURRENT APPLICATION NUMBER: US/11/135,855
; CURRENT FILING DATE: 2005-05-24
; PRIOR APPLICATION NUMBER: US/10/203,708
; PRIOR FILING DATE: 2002-08-13
; PRIOR APPLICATION NUMBER: PCT/US01/04703
; PRIOR FILING DATE: 2001-02-14
; PRIOR APPLICATION NUMBER: 60/182,172
; PRIOR FILING DATE: 2000-02-14
; PRIOR APPLICATION NUMBER: 60/186,084
; PRIOR FILING DATE: 2000-02-29
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO 44
; LENGTH: 355
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-135-855-44

Query Match 5.4%; Score 98.5; DB 7; Length 355;
Best Local Similarity 42.6%; Pred. No. 0.33;
Matches 26; Conservative 5; Mismatches 19; Indels 11; Gaps 4;
QY 263 EQQLSRKPEDESLKACVCLSPKSCVPLEGCHVSCTECTRALPEPKKPCICROA 342
DB 297 EQQLSRKPEDESLKACVCLSPKSCVPLEGCHVSCTECTRALPEPKKPCICROA 345
QY 343 I 343
DB 346 V 346

RESULT 11
US-11-069-642-137
; Sequence 137, Application US/11069642
; Publication No. US20050260626A1
; GENERAL INFORMATION:
; APPLICANT: LORENS, JAMES B.
; APPLICANT: PRAY, TODD R.
; APPLICANT: KINSELLA, TODD M.
; APPLICANT: BENNETT, MARK K.
; TITLE OF INVENTION: IN VIVO PRODUCTION OF CYCLIC PEPTIDES FOR
; TITLE OF INVENTION: INHIBITING PROTEIN-PROTEIN INTERACTION
; FILE REFERENCE: RIGI-022CIP3
; CURRENT APPLICATION NUMBER: US/11/069,642
; CURRENT FILING DATE: 2005-02-28
; PRIOR APPLICATION NUMBER: 10/232,758
; PRIOR FILING DATE: 2002-08-30
; PRIOR APPLICATION NUMBER: 10/422,536
; PRIOR FILING DATE: 2003-04-23
; PRIOR APPLICATION NUMBER: 09/800,770
; PRIOR FILING DATE: 2001-03-06
; PRIOR APPLICATION NUMBER: 60/187,130
; PRIOR FILING DATE: 2000-03-06
; NUMBER OF SEQ ID NOS: 168
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 137
; LENGTH: 491
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-069-642-137

Query Match 5.4%; Score 98.5; DB 7; Length 491;
Best Local Similarity 31.0%; Pred. No. 0.53;

Matches 27; Conservative 18; Mismatches 25; Indels 17; Gaps 5;
QY 276 QEEFHEHAQLSRKPEDESLKSA-----CVCLSPKSCVPLEGCHVSCCT 324
DB 408 QEDVKEFE-----RETDKESVSSSLPLNAIEPCVICQGRPKGCTVHGKTHLMACF 462
QY 325 ECVRALPEPKK-CPICROAIVRIPLY 350
DB 463 TCARKLKKRKNKPCVPCROPIOMIVITY 489

RESULT 12
US-11-024-959-509
; Sequence 509, Application US/11024959
; Publication No. US20060010516A1
; GENERAL INFORMATION:
; APPLICANT: FORSTER, RICHARD L.
; APPLICANT: CONNETT, MARIE B.
; APPLICANT: EMERSON, SARAH JANE
; APPLICANT: GRIGOR, MURRAY ROBERT
; APPLICANT: HIGGINS, COLLEEN M.
; APPLICANT: LUND, STEVEN TROY
; APPLICANT: MAGUSIN, ANDREAS
; APPLICANT: KODRZYCKI, BOB
; TITLE OF INVENTION: CELL CYCLE GENES AND RELATED METHODS
; FILE REFERENCE: 044463-0360
; CURRENT APPLICATION NUMBER: US/11/024,959
; CURRENT FILING DATE: 2004-12-30
; PRIOR APPLICATION NUMBER: 60/533,036
; PRIOR FILING DATE: 2003-12-30
; NUMBER OF SEQ ID NOS: 782
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 509
; LENGTH: 203
; TYPE: PRT
; ORGANISM: Pinus radiata
US-11-024-959-509

Query Match 5.4%; Score 98; DB 7; Length 203;
Best Local Similarity 31.0%; Pred. No. 0.16;
Matches 22; Conservative 16; Mismatches 29; Indels 4; Gaps 3;

QY 285 QLLSRKPEDESLKACVCLSPKSCVPLEGCHVSCTECY-RALPEPKKPCICRO- 341
DB 130 QLLSDVQSDKSEKVALTALCTSTWEERTSTICGHI-FCKKCTYNAHWRKPCICRKKL 188
QY 342 AITRVIPLYNS 352
DB 189 AINNIRIYIS 199

RESULT 13
US-10-821-234-1624
; Sequence 1624, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: PC_SEQ_genes Version 1.0
; SEQ ID NO 1624
; LENGTH: 574
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-234-1624

Query Match 5.3%; Score 97; DB 6; Length 574;
 Best Local Similarity 37.5%; Pred. No. 0.9;
 Matches 21; Conservative 4; Mismatches 23; Indels 8; Gaps 2;

QY 302 CVCCLSSFKSCVFLGCHVSCCTECYRALPEPKK-----CPICROATRYIPLYNS 352
 DB 521 CTTCYEAHADVTVITCGHMCCTVACGLRL---KKAHACCPICRPIKDIITKYRS 573

RESULT 14

US-11-072-512-2588
 ; Sequence 2588, Application US/11072512
 ; Publication No. US20060029945A1
 ; GENERAL INFORMATION:

APPLICANT: ISOGAI, TAKAO
 APPLICANT: SUGIYAMA, TOMOYASU
 APPLICANT: OTSUKI, TETSUJI
 APPLICANT: WAKAMATSU, AI
 APPLICANT: SATO, HIROYUKI
 APPLICANT: ISHII, SHIZUKO
 APPLICANT: YAMAMOTO, JUN-ICHI
 APPLICANT: ISONO, YUUKO
 APPLICANT: HIO, YURI
 APPLICANT: OTSUKA, KAORU
 APPLICANT: NAGAI, KEIICHI
 APPLICANT: IRIE, RYOTARO
 APPLICANT: TAMECHIKA, ICHIRO
 APPLICANT: SEKI, NAOHITO
 APPLICANT: YOSHIKAWA, TSUTOMU
 APPLICANT: OTSUKA, MOTYUKI
 APPLICANT: NAGAHARI, KENJI
 APPLICANT: MASUHO, YASUHIKO
 TITLE OF INVENTION: Novel full length cDNA
 FILE REFERENCE: 08435-0191
 CURRENT APPLICATION NUMBER: US/11/072,512
 PRIOR FILING DATE: 2005-03-07
 PRIOR APPLICATION NUMBER: US 60/350,978
 PRIOR FILING DATE: 2002-01-25
 PRIOR APPLICATION NUMBER: JP 2001-379298
 PRIOR FILING DATE: 2001-11-05
 NUMBER OF SEQ ID NOS: 4096
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO 2588
 LENGTH: 645
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-11-072-512-2588

Query Match 5.2%; Score 95.5; DB 7; Length 645;
 Best Local Similarity 33.3%; Pred. No. 1.4;
 Matches 26; Conservative 9; Mismatches 28; Indels 15; Gaps 4;

QY 273 KQOEFOEHQAQLLSRAKEDRESILKSACVCLSSFKSCVFLGCHVSCCTECYRALPE 332
 DB 582 RQVEELOSRYRQMEERI-----TCPICIDSHIRLVF-QCGH-GACAPCGSAL-- 627
 QY 333 PKKCPICROATRYIPLY 350
 DB 628 -SACPICROPTRIDRIOTIF 644

RESULT 15

US-11-072-512-2035
 ; Sequence 2035, Application US/11072512
 ; Publication No. US20060029945A1
 ; GENERAL INFORMATION:

APPLICANT: ISOGAI, TAKAO
 APPLICANT: SUGIYAMA, TOMOYASU
 APPLICANT: OTSUKI, TETSUJI
 APPLICANT: WAKAMATSU, AI
 APPLICANT: SATO, HIROYUKI
 APPLICANT: ISHII, SHIZUKO

APPLICANT: YAMAMOTO, JUN-ICHI
 APPLICANT: ISONO, YUUKO
 APPLICANT: HIO, YURI
 APPLICANT: OTSUKA, KAORU
 APPLICANT: NAGAI, KEIICHI
 APPLICANT: IRIE, RYOTARO
 APPLICANT: TAMECHIKA, ICHIRO
 APPLICANT: SEKI, NAOHITO
 APPLICANT: YOSHIKAWA, TSUTOMU
 APPLICANT: OTSUKA, MOTYUKI
 APPLICANT: NAGAHARI, KENJI
 APPLICANT: MASUHO, YASUHIKO
 TITLE OF INVENTION: Novel full length cDNA
 FILE REFERENCE: 08435-0191
 CURRENT APPLICATION NUMBER: US/11/072,512
 PRIOR FILING DATE: 2005-03-07
 PRIOR APPLICATION NUMBER: US 60/350,978
 PRIOR FILING DATE: 2002-01-25
 PRIOR APPLICATION NUMBER: JP 2001-379298
 PRIOR FILING DATE: 2001-11-05
 NUMBER OF SEQ ID NOS: 4096
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO 2035
 LENGTH: 670
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-11-072-512-2035

Query Match 5.1%; Score 93.5; DB 7; Length 670;
 Best Local Similarity 31.5%; Pred. No. 2.3;
 Matches 23; Conservative 13; Mismatches 28; Indels 9; Gaps 2;

QY 275 MOEFOEHQAQLLSRAKEDRESILKSACVCLSSFKSCVFLGCHVSCCTECYRALPEPK 334
 DB 109 LPEEEREPPLVFA-----EOPSVLCCQLCCSVFKDPVITTCGH---TFRCRCALKSE 159
 QY 335 KCPICROATRYI 347
 DB 160 KCPVDNVKLTIVV 172

Search completed: February 24, 2006, 08:58:09
 Job time : 19 secs

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OM protein - protein search, using sw model

Run on: February 24, 2006, 08:54:49 ; Search time 164 Seconds
(without alignments)
896.804 Million cell updates/sec

Title: US-09-978-360A-437
Perfect score: 1831
Sequence: 1 MESGRPRLCQFILGTSV.....PKCPICRAITRVILYNS 352

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA Main:
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2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.dep:*
3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.dep:*
4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.dep:*
5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.dep:*
6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.dep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1831	100.0	352	US-09-978-360A-437	Sequence 437, App
2	1831	100.0	352	US-10-024-298A-75	Sequence 75, App1
3	1831	100.0	352	US-10-042-211A-75	Sequence 75, App1
4	1831	100.0	352	US-10-315-66A-105	Sequence 105, App
5	1831	100.0	352	US-10-221-62S-25	Sequence 25, App1
6	1831	100.0	352	US-10-169-39S-92	Sequence 92, App1
7	1831	100.0	352	US-10-617-217A-75	Sequence 75, App1
8	1831	100.0	352	US-10-024-298A-75	Sequence 75, App1
9	1826	99.7	392	US-09-764-86A-801	Sequence 801, App
10	1824	99.6	352	US-10-024-298A-73	Sequence 73, App1
11	1824	99.6	352	US-10-042-211A-73	Sequence 73, App1
12	1824	99.6	352	US-10-617-217A-73	Sequence 73, App1
13	1824	99.6	352	US-10-024-298A-73	Sequence 73, App1
14	901	49.2	174	US-09-764-86A-1262	Sequence 1262, App
15	854	46.6	165	US-10-264-237-2680	Sequence 2680, App
16	442.5	24.2	338	US-11-097-143-411	Sequence 411, App
17	295	16.1	339	US-10-424-599-158556	Sequence 158556, App
18	288.5	15.8	343	US-10-425-115-364826	Sequence 364826, App
19	267.5	14.6	338	US-10-739-930-6185	Sequence 6185, App
20	262	14.3	350	US-10-425-115-364805	Sequence 364805, App
21	252.5	13.8	375	US-10-739-930-10614	Sequence 10614, App
22	231	12.6	332	US-10-425-114-47706	Sequence 47706, App
23	214	11.7	358	US-10-424-599-224671	Sequence 224671, App
24	213	11.6	310	US-10-437-963-111394	Sequence 111394, App
25	195.5	10.7	378	US-10-437-963-111394	Sequence 111394, App
26	188.5	10.3	332	US-10-195-144-83	Sequence 83, App1
27	188.5	10.3	332	US-10-345-072-83	Sequence 83, App1

28	184.5	10.1	163	US-10-425-114-65305	Sequence 65305, App
29	183	10.0	236	US-10-425-114-38446	Sequence 38446, App
30	183	10.0	236	US-10-425-115-253264	Sequence 253264, App
31	172	9.4	366	US-10-739-930-7102	Sequence 7102, App
32	163	8.9	257	US-09-949-842-14	Sequence 14, App1
33	163	8.9	403	US-10-087-192-114	Sequence 114, App1
34	155.5	8.5	303	US-10-094-749-2475	Sequence 2475, App
35	155.5	8.5	696	US-10-094-749-2425	Sequence 2425, App
36	155.5	8.5	723	US-10-104-047-2572	Sequence 2572, App
37	151	8.2	700	US-11-097-143-25191	Sequence 25191, App
38	148.5	8.1	272	US-10-108-260A-4608	Sequence 4608, App
39	145.5	7.9	336	US-10-451-168-89	Sequence 89, App1
40	145.5	7.9	336	US-10-980-387-89	Sequence 89, App1
41	144.5	7.9	169	US-10-425-115-364837	Sequence 364837, App
42	144.5	7.9	438	US-08-464-588-2	Sequence 2, App1
43	144.5	7.9	438	US-10-323-643-2	Sequence 2, App1
44	144.5	7.9	618	US-10-153-668-338	Sequence 338, App
45	144.5	7.9	618	US-10-207-655-200	Sequence 200, App

ALIGNMENTS

RESULT 1
US-09-978-360A-437

Sequence 437, Application US/0978360A
Publication No. US20040110939A1

GENERAL INFORMATION:

APPLICANT: Edwards, Jean-Baptiste Dumas Milne

APPLICANT: Ductier, Aymeric

APPLICANT: Bougueleret, Lydie

APPLICANT: Jobert, Severin

APPLICANT: Clusel, Catherine

TITLE OF INVENTION: Complementary DNA's Encoding Proteins with Signal Peptides

FILE REFERENCE: 56, US4, CIP

CURRENT APPLICATION NUMBER: US/09/978,360A

PRIOR FILING DATE: 2001-10-15

PRIOR APPLICATION NUMBER: US 60/066,677

PRIOR FILING DATE: 1997-11-13

PRIOR APPLICATION NUMBER: US 60/069,957

PRIOR FILING DATE: 1997-12-17

PRIOR APPLICATION NUMBER: US 60/074,121

PRIOR FILING DATE: 1998-02-09

PRIOR APPLICATION NUMBER: US 60/081,563

PRIOR FILING DATE: 1998-04-13

PRIOR APPLICATION NUMBER: US 60/096,116

PRIOR FILING DATE: 1998-08-10

PRIOR APPLICATION NUMBER: US 60/099,273

PRIOR FILING DATE: -09-04

PRIOR APPLICATION NUMBER: US 09/191,997

PRIOR FILING DATE: 1998-11-13

PRIOR APPLICATION NUMBER: US 09/215,435

PRIOR FILING DATE: 1998-12-17

PRIOR APPLICATION NUMBER: PCT/IB98/02122

PRIOR FILING DATE: 1998-12-17

PRIOR APPLICATION NUMBER: US 09/247,155

PRIOR FILING DATE: 1999-02-09

Remaining Prior Application data removed - See File Wrapper or PALM.

NUMBER OF SEQ ID NOS: 810

SOFTWARE: Patent.pm

SEQ ID NO 437

LENGTH: 352

TYPE: PRT

ORGANISM: Homo Sapiens

FEATURE:

NAME/KEY: SIGNAL

LOCATION: -23...-1

US-09-978-360A-437

Query Match

Best Local Similarity 100.0%; Score 1831; DB 3; Length 352;

Mismatches 352; Conservative 0; Indels 0; Gaps 0;

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QY 1 MESSGRPSLCOFILIGTTSVYTAALYSYRQKARVSQELKGAKVHIGEDLKSILSEAPG 60
DB 1 MESSGRPSLCOFILIGTTSVYTAALYSYRQKARVSQELKGAKVHIGEDLKSILSEAPG 60
QY 61 KCVPAVAVIEGAVRSVKEITLNSQFVENCCKGVIQRLTLOEHKVMWNRTHLMNDCSKIITHOR 120
DB 61 KCVPAVAVIEGAVRSVKEITLNSQFVENCCKGVIQRLTLOEHKVMWNRTHLMNDCSKIITHOR 120
QY 121 TINTVPFDLVPHEDGDVAVRVLKPLDSVDLGLFTVYEKFPHSIOSFTDVIIGHYISGERPK 180
DB 121 TINTVPFDLVPHEDGDVAVRVLKPLDSVDLGLFTVYEKFPHSIOSFTDVIIGHYISGERPK 180
QY 181 GIOETEBMLKVGAATLTGVGELVLDNNSVRLQPKQMOQYIYSQDPFSLQROESSVRLW 240
DB 181 GIOETEBMLKVGAATLTGVGELVLDNNSVRLQPKQMOQYIYSQDPFSLQROESSVRLW 240
QY 241 KVALVVGFPATCATLFFILRKQYLOQROERLRLKQMOEFQEHBAQLLSRAKPEDRESLKS 300
DB 241 KVALVVGFPATCATLFFILRKQYLOQROERLRLKQMOEFQEHBAQLLSRAKPEDRESLKS 300
QY 301 ACVVCLSFFKSCVFLIECGHVCSCTECYRALPEPKKCPICROAITRVIPLVNS 352
DB 301 ACVVCLSFFKSCVFLIECGHVCSCTECYRALPEPKKCPICROAITRVIPLVNS 352

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RESULT 2

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US-10-024-298A-75
; Sequence 75, Application US/10024298A
; Publication No. US20030143540A1
; GENERAL INFORMATION:
; APPLICANT: ASAMI KASEI KABUSHIKI KAISHA
; APPLICANT: AKIO MATSUDA
; APPLICANT: Goichi HONDA
; APPLICANT: Shuji MURAMATSU
; APPLICANT: YUKIKO NAGANO
; TITLE OF INVENTION: NP-K-B Activating Gene
; FILE REFERENCE: 1254-0191P
; CURRENT APPLICATION NUMBER: US/10/024,298A
; PRIOR FILING DATE: 2003-04-08
; PRIOR APPLICATION NUMBER: 60/314,385
; PRIOR FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: 60/278,641
; PRIOR FILING DATE: 2001-03-26
; PRIOR APPLICATION NUMBER: 60/258,315
; PRIOR FILING DATE: 2000-12-28
; PRIOR APPLICATION NUMBER: JP254018/2001
; PRIOR FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: JP0088912/2001
; PRIOR FILING DATE: 2001-03-26
; PRIOR APPLICATION NUMBER: JP402288/2000
; PRIOR FILING DATE: 2000-12-28
; NUMBER OF SEQ ID NOS: 182
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 75
; LENGTH: 352
; TYPE: PRF
; ORGANISM: Homo sapiens
US-10-024-298A-75

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Query Match 100.0%; Score 1831; DB 4; Length 352;
Best Local Similarity 100.0%; Pred. No. 1,1e-162;
Matches 352; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MESSGRPSLCOFILIGTTSVYTAALYSYRQKARVSQELKGAKVHIGEDLKSILSEAPG 60
DB 1 MESSGRPSLCOFILIGTTSVYTAALYSYRQKARVSQELKGAKVHIGEDLKSILSEAPG 60
QY 61 KCVPAVAVIEGAVRSVKEITLNSQFVENCCKGVIQRLTLOEHKVMWNRTHLMNDCSKIITHOR 120
DB 61 KCVPAVAVIEGAVRSVKEITLNSQFVENCCKGVIQRLTLOEHKVMWNRTHLMNDCSKIITHOR 120
QY 121 TINTVPFDLVPHEDGDVAVRVLKPLDSVDLGLFTVYEKFPHSIOSFTDVIIGHYISGERPK 180
DB 121 TINTVPFDLVPHEDGDVAVRVLKPLDSVDLGLFTVYEKFPHSIOSFTDVIIGHYISGERPK 180

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DB 121 TINTVPFDLVPHEDGDVAVRVLKPLDSVDLGLFTVYEKFPHSIOSFTDVIIGHYISGERPK 180
QY 181 GIOETEBMLKVGAATLTGVGELVLDNNSVRLQPKQMOQYIYSQDPFSLQROESSVRLW 240
DB 181 GIOETEBMLKVGAATLTGVGELVLDNNSVRLQPKQMOQYIYSQDPFSLQROESSVRLW 240
QY 241 KVALVVGFPATCATLFFILRKQYLOQROERLRLKQMOEFQEHBAQLLSRAKPEDRESLKS 300
DB 241 KVALVVGFPATCATLFFILRKQYLOQROERLRLKQMOEFQEHBAQLLSRAKPEDRESLKS 300
QY 301 ACVVCLSFFKSCVFLIECGHVCSCTECYRALPEPKKCPICROAITRVIPLVNS 352
DB 301 ACVVCLSFFKSCVFLIECGHVCSCTECYRALPEPKKCPICROAITRVIPLVNS 352

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RESULT 3

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US-10-042-211A-75
; Sequence 75, Application US/10042211A
; Publication No. US20030170719A1
; GENERAL INFORMATION:
; APPLICANT: MATSUDA, AKIO et al.
; TITLE OF INVENTION: NFKB Activating Gene
; FILE REFERENCE: 1254-0192P
; CURRENT APPLICATION NUMBER: US/10/042,211A
; PRIOR FILING DATE: 2002-01-11
; PRIOR APPLICATION NUMBER: JP 2000-402288
; PRIOR FILING DATE: 2000-12-28
; PRIOR APPLICATION NUMBER: JP 2001-088912
; PRIOR FILING DATE: 2001-03-26
; PRIOR APPLICATION NUMBER: JP 2001-254018
; PRIOR FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: US 60/258,315
; PRIOR FILING DATE: 2000-12-28
; PRIOR APPLICATION NUMBER: US 60/278,640
; PRIOR FILING DATE: 2001-03-26
; PRIOR APPLICATION NUMBER: US 60/314,385
; PRIOR FILING DATE: 2001-08-24
; NUMBER OF SEQ ID NOS: 182
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 75
; LENGTH: 352
; TYPE: PRF
; ORGANISM: Homo sapiens
US-10-042-211A-75

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Query Match 100.0%; Score 1831; DB 4; Length 352;
Best Local Similarity 100.0%; Pred. No. 1,1e-162;
Matches 352; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MESSGRPSLCOFILIGTTSVYTAALYSYRQKARVSQELKGAKVHIGEDLKSILSEAPG 60
DB 1 MESSGRPSLCOFILIGTTSVYTAALYSYRQKARVSQELKGAKVHIGEDLKSILSEAPG 60
QY 61 KCVPAVAVIEGAVRSVKEITLNSQFVENCCKGVIQRLTLOEHKVMWNRTHLMNDCSKIITHOR 120
DB 61 KCVPAVAVIEGAVRSVKEITLNSQFVENCCKGVIQRLTLOEHKVMWNRTHLMNDCSKIITHOR 120
QY 121 TINTVPFDLVPHEDGDVAVRVLKPLDSVDLGLFTVYEKFPHSIOSFTDVIIGHYISGERPK 180
DB 121 TINTVPFDLVPHEDGDVAVRVLKPLDSVDLGLFTVYEKFPHSIOSFTDVIIGHYISGERPK 180
QY 181 GIOETEBMLKVGAATLTGVGELVLDNNSVRLQPKQMOQYIYSQDPFSLQROESSVRLW 240
DB 181 GIOETEBMLKVGAATLTGVGELVLDNNSVRLQPKQMOQYIYSQDPFSLQROESSVRLW 240
QY 241 KVALVVGFPATCATLFFILRKQYLOQROERLRLKQMOEFQEHBAQLLSRAKPEDRESLKS 300
DB 241 KVALVVGFPATCATLFFILRKQYLOQROERLRLKQMOEFQEHBAQLLSRAKPEDRESLKS 300
QY 301 ACVVCLSFFKSCVFLIECGHVCSCTECYRALPEPKKCPICROAITRVIPLVNS 352
DB 301 ACVVCLSFFKSCVFLIECGHVCSCTECYRALPEPKKCPICROAITRVIPLVNS 352

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RESULT 4
US-10-315-664-105
; Sequence 105, Application US/10315664
; Publication No. US20030203377A1
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Bouguetieret, L.
; APPLICANT: Jobert, S.
; TITLE OF INVENTION: Complementary DNA's Encoding Proteins with Signal
; FILE REFERENCE: GENSET.050CP3
; CURRENT APPLICATION NUMBER: US/10/315,664
; CURRENT FILING DATE: 2002-12-09
; PRIOR APPLICATION NUMBER: US/09/599,360
; PRIOR FILING DATE: 2000-06-21
; PRIOR APPLICATION NUMBER: 60/113,686
; PRIOR FILING DATE: 1998-12-22
; PRIOR APPLICATION NUMBER: 60/141,032
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: 09/469,099
; PRIOR FILING DATE: 1999-12-21
; NUMBER OF SEQ ID NOS: 123
; SOFTWARE: Patent.pm
; SEQ ID NO 105
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: -23...-1
US-10-315-664-105

Query Match          100.0%; Score 1831; DB 4; Length 352;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
Matches 352; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MESGRPSLCOFILIGTTSVTTAALYSYRQKARVSQELKAKVHLEBDLSISEAPG 60
DB 1 MESGRPSLCOFILIGTTSVTTAALYSYRQKARVSQELKAKVHLEBDLSISEAPG 60
QY 61 KCVPAVAVEGAVRSYKETLNSQFVENCCKGVORLTLOEHKVMWNRTHLMDCKIIR 120
DB 61 KCVPAVAVEGAVRSYKETLNSQFVENCCKGVORLTLOEHKVMWNRTHLMDCKIIR 120
QY 121 TMTVPFDLVPHEDGDVAVRVLKPLDSVDLGLETYEKHPHSIQSFDTVIGHYISGERPK 180
DB 121 TMTVPFDLVPHEDGDVAVRVLKPLDSVDLGLETYEKHPHSIQSFDTVIGHYISGERPK 180
QY 181 GIQTEEMLKVGATLTGVELVLDNNSVRLQPPKQGMYYLSSQDFSLQROESSVRLM 240
DB 181 GIQTEEMLKVGATLTGVELVLDNNSVRLQPPKQGMYYLSSQDFSLQROESSVRLM 240
QY 241 KVLAVFGFATCATLFFILRKQYLOEROERLRLKQMOEFQHEAQLLSRAKPEDRESLKS 300
DB 241 KVLAVFGFATCATLFFILRKQYLOEROERLRLKQMOEFQHEAQLLSRAKPEDRESLKS 300
QY 301 ACVCLISFKSCVPLECGHVCSTECYRALPEPKKCPICROAITRVIPLYNS 352
DB 301 ACVCLISFKSCVPLECGHVCSTECYRALPEPKKCPICROAITRVIPLYNS 352

RESULT 5
US-10-221-625-25
; Sequence 25, Application US/10221625
; Publication No. US20040033942A1
; GENERAL INFORMATION:
; APPLICANT: INCYTE GENOMICS, INC.
; APPLICANT: HILMAN, Jennifer L.
; APPLICANT: BAUGHN, Mariah R.
; APPLICANT: YUE, Henry
; APPLICANT: LAL, Preeti
; APPLICANT: LU, Dying Aina M.

```

```

; APPLICANT: PATTERSON, Chandra
; APPLICANT: AZIMZAI, Yalda
; APPLICANT: BANDMAN, Olga
; APPLICANT: TANG, Y. Tom
; APPLICANT: MATHUR, Preeti
; APPLICANT: SHAH, Puri
; APPLICANT: AU-YOUNG, Janice
; APPLICANT: REDDY, Roopa
; TITLE OF INVENTION: TRANSCRIPTION FACTORS
; FILE REFERENCE: PF-0761 PCT
; CURRENT APPLICATION NUMBER: US/10/221,625
; CURRENT FILING DATE: 2001-03-13
; NUMBER OF SEQ ID NOS: 214
; SOFTWARE: PERL Program
; SEQ ID NO 25
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20040033942A1 1383473CD1
US-10-221-625-25

Query Match          100.0%; Score 1831; DB 4; Length 352;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
Matches 352; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MESGRPSLCOFILIGTTSVTTAALYSYRQKARVSQELKAKVHLEBDLSISEAPG 60
DB 1 MESGRPSLCOFILIGTTSVTTAALYSYRQKARVSQELKAKVHLEBDLSISEAPG 60
QY 61 KCVPAVAVEGAVRSYKETLNSQFVENCCKGVORLTLOEHKVMWNRTHLMDCKIIR 120
DB 61 KCVPAVAVEGAVRSYKETLNSQFVENCCKGVORLTLOEHKVMWNRTHLMDCKIIR 120
QY 121 TMTVPFDLVPHEDGDVAVRVLKPLDSVDLGLETYEKHPHSIQSFDTVIGHYISGERPK 180
DB 121 TMTVPFDLVPHEDGDVAVRVLKPLDSVDLGLETYEKHPHSIQSFDTVIGHYISGERPK 180
QY 181 GIQTEEMLKVGATLTGVELVLDNNSVRLQPPKQGMYYLSSQDFSLQROESSVRLM 240
DB 181 GIQTEEMLKVGATLTGVELVLDNNSVRLQPPKQGMYYLSSQDFSLQROESSVRLM 240
QY 241 KVLAVFGFATCATLFFILRKQYLOEROERLRLKQMOEFQHEAQLLSRAKPEDRESLKS 300
DB 241 KVLAVFGFATCATLFFILRKQYLOEROERLRLKQMOEFQHEAQLLSRAKPEDRESLKS 300
QY 301 ACVCLISFKSCVPLECGHVCSTECYRALPEPKKCPICROAITRVIPLYNS 352
DB 301 ACVCLISFKSCVPLECGHVCSTECYRALPEPKKCPICROAITRVIPLYNS 352

RESULT 6
US-10-169-395-92
; Sequence 92, Application US/10169395
; Publication No. US20040034192A1
; GENERAL INFORMATION:
; APPLICANT: KATO, Seishi
; APPLICANT: KIMURA, Tomoko
; TITLE OF INVENTION: HUMAN PROTEINS HAVING HYDROPHOBIC DOMAINS AND DNAs ENCODING
; FILE REFERENCE: 01997.015100.US
; CURRENT APPLICATION NUMBER: US/10/169,395
; CURRENT FILING DATE: 2002-11-29
; PRIOR APPLICATION NUMBER: JP 2000-585
; PRIOR FILING DATE: 2000-01-06
; PRIOR APPLICATION NUMBER: JP 2000-588
; PRIOR FILING DATE: 2000-01-06
; PRIOR APPLICATION NUMBER: JP 2000-2299
; PRIOR FILING DATE: 2000-01-11
; PRIOR APPLICATION NUMBER: JP 2000-26862
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: JP 2000-58367

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;; PRIOR FILING DATE: 2000-03-03
 ;; PRIOR APPLICATION NUMBER: PCT/JP00/09359
 ;; PRIOR FILING DATE: 2000-12-28
 ;; NUMBER OF SEQ ID NOS: 150
 ;; SEQ ID NO 92
 ;; LENGTH: 352
 ;; TYPE: PRT
 ;; ORGANISM: Homo sapiens
 US-10-169-395-92

Query Match
 Best Local Similarity 100.0%; Score 1831; DB 4; Length 352;
 Matches 352; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MESGGRPSLCQFILLGTTSVVTAALYSVYRQKARVSQELKGAKVHLSGEDLSIISAPG 60
 DB 1 MESGGRPSLCQFILLGTTSVVTAALYSVYRQKARVSQELKGAKVHLSGEDLSIISAPG 60
 QY 61 KCPYAVIBGAVRSVKEETINSQFVENCCKGVIQRLTLOEHKVMNRTTHLMDCKSIHQR 120
 DB 61 KCPYAVIBGAVRSVKEETINSQFVENCCKGVIQRLTLOEHKVMNRTTHLMDCKSIHQR 120
 QY 121 TMTVPFDLVPHEDGVAVRVLKPLDSVDLGLETYEKFPHSIQSFVDVIGHYISGERPK 180
 DB 121 TMTVPFDLVPHEDGVAVRVLKPLDSVDLGLETYEKFPHSIQSFVDVIGHYISGERPK 180
 QY 181 GIOETEEMLKVGATLTGVELVDNNSVRLQPPKQMGYYLSQDFSLQROESSVRLW 240
 DB 181 GIOETEEMLKVGATLTGVELVDNNSVRLQPPKQMGYYLSQDFSLQROESSVRLW 240
 QY 241 KYLAVFGPATCATLFFILRKQYLORERLRLKQOEFOHEAQLLSRAKPEDRESLKS 300
 DB 241 KYLAVFGPATCATLFFILRKQYLORERLRLKQOEFOHEAQLLSRAKPEDRESLKS 300
 QY 301 ACVVCISFSCVFLGCGHVCCTECYRALPEPKKCPICROATIRVIPLVNS 352
 DB 301 ACVVCISFSCVFLGCGHVCCTECYRALPEPKKCPICROATIRVIPLVNS 352

RESULT 7

US-10-617-217A-75
 ; Sequence 75, Application US/10617217A
 ; Publication No. US20040081986A1
 ; GENERAL INFORMATION:
 ; APPLICANT: MATSUDA, Akio et al.
 ; TITLE OF INVENTION: NF-kB ACTIVATING GENE
 ; FILE REFERENCE: 1254-0229P
 ; CURRENT APPLICATION NUMBER: US/10/617, 217A
 ; PRIOR FILING DATE: 2003-07-11
 ; PRIOR APPLICATION NUMBER: JP 2000-402288
 ; PRIOR FILING DATE: 2000-12-28
 ; PRIOR APPLICATION NUMBER: JP 2001-088912
 ; PRIOR FILING DATE: 2001-03-26
 ; PRIOR APPLICATION NUMBER: JP 2001-254018
 ; PRIOR FILING DATE: 2001-08-24
 ; PRIOR APPLICATION NUMBER: US 60/258,315
 ; PRIOR FILING DATE: 2000-12-28
 ; PRIOR APPLICATION NUMBER: US 60/278,640
 ; PRIOR FILING DATE: 2001-03-26
 ; PRIOR APPLICATION NUMBER: US 60/314,385
 ; NUMBER OF SEQ ID NOS: 224
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 75
 ; LENGTH: 352
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-617-217A-75

Query Match
 Best Local Similarity 100.0%; Score 1831; DB 4; Length 352;
 Matches 352; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MESGGRPSLCQFILLGTTSVVTAALYSVYRQKARVSQELKGAKVHLSGEDLSIISAPG 60
 DB 1 MESGGRPSLCQFILLGTTSVVTAALYSVYRQKARVSQELKGAKVHLSGEDLSIISAPG 60
 QY 61 KCPYAVIBGAVRSVKEETINSQFVENCCKGVIQRLTLOEHKVMNRTTHLMDCKSIHQR 120
 DB 61 KCPYAVIBGAVRSVKEETINSQFVENCCKGVIQRLTLOEHKVMNRTTHLMDCKSIHQR 120
 QY 121 TMTVPFDLVPHEDGVAVRVLKPLDSVDLGLETYEKFPHSIQSFVDVIGHYISGERPK 180
 DB 121 TMTVPFDLVPHEDGVAVRVLKPLDSVDLGLETYEKFPHSIQSFVDVIGHYISGERPK 180
 QY 181 GIOETEEMLKVGATLTGVELVDNNSVRLQPPKQMGYYLSQDFSLQROESSVRLW 240
 DB 181 GIOETEEMLKVGATLTGVELVDNNSVRLQPPKQMGYYLSQDFSLQROESSVRLW 240
 QY 241 KYLAVFGPATCATLFFILRKQYLORERLRLKQOEFOHEAQLLSRAKPEDRESLKS 300
 DB 241 KYLAVFGPATCATLFFILRKQYLORERLRLKQOEFOHEAQLLSRAKPEDRESLKS 300
 QY 301 ACVVCISFSCVFLGCGHVCCTECYRALPEPKKCPICROATIRVIPLVNS 352
 DB 301 ACVVCISFSCVFLGCGHVCCTECYRALPEPKKCPICROATIRVIPLVNS 352

RESULT 8

US-10-024-298A-75
 ; Sequence 75, Application US/10024298A
 ; Publication No. US2004021467A9
 ; GENERAL INFORMATION:
 ; APPLICANT: ASAH KASEI KABUSHIKI KAISHA
 ; APPLICANT: AKIO MATSUDA
 ; APPLICANT: Goichi HONDA
 ; APPLICANT: Shuji MURAMATSU
 ; APPLICANT: Yukiko NAGANO
 ; TITLE OF INVENTION: NF-kB Activating Gene
 ; FILE REFERENCE: 1254-0191P
 ; CURRENT APPLICATION NUMBER: US/10/024, 298A
 ; PRIOR FILING DATE: 2003-04-08
 ; PRIOR APPLICATION NUMBER: 60/314,385
 ; PRIOR FILING DATE: 2001-08-24
 ; PRIOR APPLICATION NUMBER: 60/278,641
 ; PRIOR FILING DATE: 2001-03-26
 ; PRIOR APPLICATION NUMBER: 60/258,315
 ; PRIOR FILING DATE: 2000-12-28
 ; PRIOR APPLICATION NUMBER: JP254018/2001
 ; PRIOR FILING DATE: 2001-08-24
 ; PRIOR APPLICATION NUMBER: JP0088912/2001
 ; PRIOR FILING DATE: 2001-03-26
 ; PRIOR APPLICATION NUMBER: JP402288/2000
 ; NUMBER OF SEQ ID NOS: 182
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 75
 ; LENGTH: 352
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-024-298A-75

Query Match
 Best Local Similarity 100.0%; Score 1831; DB 4; Length 352;
 Matches 352; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MESGGRPSLCQFILLGTTSVVTAALYSVYRQKARVSQELKGAKVHLSGEDLSIISAPG 60
 DB 1 MESGGRPSLCQFILLGTTSVVTAALYSVYRQKARVSQELKGAKVHLSGEDLSIISAPG 60
 QY 61 KCPYAVIBGAVRSVKEETINSQFVENCCKGVIQRLTLOEHKVMNRTTHLMDCKSIHQR 120
 DB 61 KCPYAVIBGAVRSVKEETINSQFVENCCKGVIQRLTLOEHKVMNRTTHLMDCKSIHQR 120
 QY 121 TMTVPFDLVPHEDGVAVRVLKPLDSVDLGLETYEKFPHSIQSFVDVIGHYISGERPK 180
 DB 121 TMTVPFDLVPHEDGVAVRVLKPLDSVDLGLETYEKFPHSIQSFVDVIGHYISGERPK 180

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Db      121 TTTVPFDLVPHEDGVDAVAVRLKPLDSVDLGLETYEKHPISQSFDTVIGHYISGERPK 180
Qy      181 G|O|E|E|M|K|G|A|T|T|G|E|L|V|D|N|N|S|V|R|O|P|K|G|M|O|Y|L|S|S|O|P|D|S|L|O|Q|E|S|V|R|L| 240
        181 G|O|E|E|M|K|G|A|T|T|G|E|L|V|D|N|N|S|V|R|O|P|K|G|M|O|Y|L|S|S|O|P|D|S|L|O|Q|E|S|V|R|L| 240
Qy      241 K|T|A|V|F|G|P|A|T|C|A|T|F|I|L|R|K|O|Y|L|O|R|O|E|R|L|K|O|Q|E|F|O|E|H|A|O|L|S|R|A|K|P|E|D|R|E|S|L|K|S| 300
        241 K|T|A|V|F|G|P|A|T|C|A|T|F|I|L|R|K|O|Y|L|O|R|O|E|R|L|K|O|Q|E|F|O|E|H|A|O|L|S|R|A|K|P|E|D|R|E|S|L|K|S| 300
Db      301 A|C|V|C|L|S|F|K|S|C|V|F|E|C|G|H|V|C|T|E|C|Y|R|A|L|P|E|P|K|C|P|I|C|R|O|A|I|T|R|V|I|P|L|Y|N|S| 352
        301 A|C|V|C|L|S|F|K|S|C|V|F|E|C|G|H|V|C|T|E|C|Y|R|A|L|P|E|P|K|C|P|I|C|R|O|A|I|T|R|V|I|P|L|Y|N|S| 352

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RESULT 9
US-09-764-864-801
Sequence 801, Application US/09764864
Patent No. US20020132753A1
GENERAL INFORMATION:

APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PT223
CURRENT APPLICATION NUMBER: US/09/764,864
CURRENT FILING DATE: 2001-01-17
Prior application data removed - consult PALM or file wrapper
NUMBER OF SEQ ID NOS: 1792
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 801
LENGTH: 392
TYPE: PRT
ORGANISM: Homo sapiens

FEATURE: NAME/KEY: SITE
LOCATION: (238)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-764-864-801

Query Match 99.7%; Score 1826; DB 3; Length 392;
Best Local Similarity 99.7%; Pred. No. 3.7e-162;
Matches 351; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy      1 M|E|S|G|R|P|S|C|O|P|I|L|G|T|S|V|T|A|L|Y|S|V|R|O|K|A|R|V|S|O|E|L|K|G|K|K|H|L|G|D|L|K|S|I|S|E|A|G| 60
        41 M|E|S|G|R|P|S|C|O|P|I|L|G|T|S|V|T|A|L|Y|S|V|R|O|K|A|R|V|S|O|E|L|K|G|K|K|H|L|G|D|L|K|S|I|S|E|A|G| 100
Db      61 K|C|P|A|V|A|E|G|A|R|S|V|E|T|I|N|S|Q|F|E|N|C|K|G|V|O|R|L|T|O|E|H|K|W|N|R|T|H|L|M|N|D|S|K|I|H|O|R| 120
        101 K|C|P|A|V|A|E|G|A|R|S|V|E|T|I|N|S|Q|F|E|N|C|K|G|V|O|R|L|T|O|E|H|K|W|N|R|T|H|L|M|N|D|S|K|I|H|O|R| 160
Qy      121 T|T|T|V|P|D|L|V|P|H|E|D|G|V|D|A|V|R|L|K|P|L|D|S|V|D|L|G|E|T|Y|E|K|H|P|S|I|Q|S|F|T|D|V|I|G|H|Y|I|S|G|E|R|P|K| 180
        161 T|T|T|V|P|D|L|V|P|H|E|D|G|V|D|A|V|R|L|K|P|L|D|S|V|D|L|G|E|T|Y|E|K|H|P|S|I|Q|S|F|T|D|V|I|G|H|Y|I|S|G|E|R|P|K| 220
Db      181 G|O|E|E|M|K|G|A|T|T|G|E|L|V|D|N|N|S|V|R|O|P|K|G|M|O|Y|L|S|S|O|P|D|S|L|O|Q|E|S|V|R|L| 240
        221 G|O|E|E|M|K|G|A|T|T|G|E|L|V|D|N|N|S|V|R|O|P|K|G|M|O|Y|L|S|S|O|P|D|S|L|O|Q|E|S|V|R|L| 280
Qy      241 K|T|A|V|F|G|P|A|T|C|A|T|F|I|L|R|K|O|Y|L|O|R|O|E|R|L|K|O|Q|E|F|O|E|H|A|O|L|S|R|A|K|P|E|D|R|E|S|L|K|S| 300
        281 K|T|A|V|F|G|P|A|T|C|A|T|F|I|L|R|K|O|Y|L|O|R|O|E|R|L|K|O|Q|E|F|O|E|H|A|O|L|S|R|A|K|P|E|D|R|E|S|L|K|S| 340
Db      301 A|C|V|C|L|S|F|K|S|C|V|F|E|C|G|H|V|C|T|E|C|Y|R|A|L|P|E|P|K|C|P|I|C|R|O|A|I|T|R|V|I|P|L|Y|N|S| 352
        341 A|C|V|C|L|S|F|K|S|C|V|F|E|C|G|H|V|C|T|E|C|Y|R|A|L|P|E|P|K|C|P|I|C|R|O|A|I|T|R|V|I|P|L|Y|N|S| 392

```

RESULT 10
US-10-024-298A-73
Sequence 73, Application US/10024298A
Publication No. US20030143540A1
GENERAL INFORMATION:
APPLICANT: ASAMI KASEI KABUSHIKI KAISHA

```

; APPLICANT: AKIO MATSUDA
; APPLICANT: GOICHI HONDA
; APPLICANT: SHUJI MURAMATSU
; APPLICANT: YUKIKO NAGANO
; FILE REFERENCE: 1254-0191P
; CURRENT APPLICATION NUMBER: US/10/024,298A
; CURRENT FILING DATE: 2003-04-08
; PRIOR APPLICATION NUMBER: 60/314,385
; PRIOR FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: 60/278,641
; PRIOR FILING DATE: 2001-03-26
; PRIOR APPLICATION NUMBER: 60/258,315
; PRIOR FILING DATE: 2000-12-28
; PRIOR APPLICATION NUMBER: JP254018/2001
; PRIOR FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: JP0088912/2001
; PRIOR FILING DATE: 2001-03-26
; PRIOR APPLICATION NUMBER: JP402288/2000
; PRIOR FILING DATE: 2000-12-28
; NUMBER OF SEQ ID NOS: 182
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 73
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-024-298A-73

```

Query Match 99.6%; Score 1824; DB 4; Length 352;
Best Local Similarity 99.7%; Pred. No. 4.9e-162;
Matches 351; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy      1 M|E|S|G|R|P|S|C|O|P|I|L|G|T|S|V|T|A|L|Y|S|V|R|O|K|A|R|V|S|O|E|L|K|G|K|K|H|L|G|D|L|K|S|I|S|E|A|G| 60
        1 M|E|S|G|R|P|S|C|O|P|I|L|G|T|S|V|T|A|L|Y|S|V|R|O|K|A|R|V|S|O|E|L|K|G|K|K|H|L|G|D|L|K|S|I|S|E|A|G| 60
Db      61 K|C|P|A|V|A|E|G|A|R|S|V|E|T|I|N|S|Q|F|E|N|C|K|G|V|O|R|L|T|O|E|H|K|W|N|R|T|H|L|M|N|D|S|K|I|H|O|R| 120
        61 K|C|P|A|V|A|E|G|A|R|S|V|E|T|I|N|S|Q|F|E|N|C|K|G|V|O|R|L|T|O|E|H|K|W|N|R|T|H|L|M|N|D|S|K|I|H|O|R| 120
Qy      121 T|T|T|V|P|D|L|V|P|H|E|D|G|V|D|A|V|R|L|K|P|L|D|S|V|D|L|G|E|T|Y|E|K|H|P|S|I|Q|S|F|T|D|V|I|G|H|Y|I|S|G|E|R|P|K| 180
        121 T|T|T|V|P|D|L|V|P|H|E|D|G|V|D|A|V|R|L|K|P|L|D|S|V|D|L|G|E|T|Y|E|K|H|P|S|I|Q|S|F|T|D|V|I|G|H|Y|I|S|G|E|R|P|K| 180
Db      181 G|O|E|E|M|K|G|A|T|T|G|E|L|V|D|N|N|S|V|R|O|P|K|G|M|O|Y|L|S|S|O|P|D|S|L|O|Q|E|S|V|R|L| 240
        181 G|O|E|E|M|K|G|A|T|T|G|E|L|V|D|N|N|S|V|R|O|P|K|G|M|O|Y|L|S|S|O|P|D|S|L|O|Q|E|S|V|R|L| 240
Qy      241 K|T|A|V|F|G|P|A|T|C|A|T|F|I|L|R|K|O|Y|L|O|R|O|E|R|L|K|O|Q|E|F|O|E|H|A|O|L|S|R|A|K|P|E|D|R|E|S|L|K|S| 300
        241 K|T|A|V|F|G|P|A|T|C|A|T|F|I|L|R|K|O|Y|L|O|R|O|E|R|L|K|O|Q|E|F|O|E|H|A|O|L|S|R|A|K|P|E|D|R|E|S|L|K|S| 300
Db      301 A|C|V|C|L|S|F|K|S|C|V|F|E|C|G|H|V|C|T|E|C|Y|R|A|L|P|E|P|K|C|P|I|C|R|O|A|I|T|R|V|I|P|L|Y|N|S| 352
        301 A|C|V|C|L|S|F|K|S|C|V|F|E|C|G|H|V|C|T|E|C|Y|R|A|L|P|E|P|K|C|P|I|C|R|O|A|I|T|R|V|I|P|L|Y|N|S| 352

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RESULT 11
US-10-042-211A-73
Sequence 73, Application US/10042211A
Publication No. US20030170719A1
GENERAL INFORMATION:
APPLICANT: MATSUDA, AKIO et al.
TITLE OF INVENTION: NF-κB Activating Gene
FILE REFERENCE: 1254-0192P
CURRENT APPLICATION NUMBER: US/10/042,211A
CURRENT FILING DATE: 2002-01-11
PRIOR APPLICATION NUMBER: JP 2000-402288
PRIOR FILING DATE: 2000-12-28
PRIOR APPLICATION NUMBER: JP 2001-088912
PRIOR FILING DATE: 2001-03-26
PRIOR APPLICATION NUMBER: JP 2001-254018
PRIOR FILING DATE: 2001-08-24

PRIOR APPLICATION NUMBER: US 60/258,315
PRIOR FILING DATE: 2000-12-28
PRIOR APPLICATION NUMBER: US 60/278,640
PRIOR FILING DATE: 2001-03-26
PRIOR APPLICATION NUMBER: US 60/314,385
PRIOR FILING DATE: 2001-08-24
NUMBER OF SEQ ID NOS: 182
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 73
LENGTH: 352
TYPE: PRT
ORGANISM: Homo sapiens
US-10-042-211A-73

Query Match 99.6%; Score 1824; DB 4; Length 352;
Best Local Similarity 99.7%; Pred. No. 4.9e-162;
Matches 351; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MESSGRPSLCQFILGTTSVVTAALYSYVRQKARVSGELKGAKKVLGEDLKSILSEAPG 60
DB 1 MESSGRPSLCQFILGTTSVVTAALYSYVRQKARVSGELKGAKKVLGEDLKSILSEAPG 60
QY 61 KCVPAVIEGAVRSYKETLNSQFVENCCKGVIGRLTLOEHKVMNRTTHLMDCKIHHOR 120
DB 61 KCVPAVIEGAVRSYKETLNSQFVENCCKGVIGRLTLOEHKVMNRTTHLMDCKIHHOR 120
QY 121 TMTVPDLVPHEDGDVAARVVKPLDSVDLGLETYKFKPFSIOSFTDVI GHYISGERPK 180
DB 121 TMTVPDLVPHEDGDVAARVVKPLDSVDLGLETYKFKPFSIOSFTDVI GHYISGERPK 180
QY 181 GIOETEMLVKVGATLTGVELVDNNSVRLQPPKQMGVYLLSQDFDLSLQROESSVRLM 240
DB 181 GIOETEMLVKVGATLTGVELVDNNSVRLQPPKQMGVYLLSQDFDLSLQROESSVRLM 240
QY 241 KVLALVFGPATCATLFFILRKQYLORQERLRLKQOEFOEHEAQLLSRAKPEDRESLKS 300
DB 241 KVLALVFGPATCATLFFILRKQYLORQERLRLKQOEFOEHEAQLLSRAKPEDRESLKS 300
QY 301 ACVCLSSPKSCVFLKCGHVCSTECYRALPEPKKCPICROAITRVIPIYNS 352
DB 301 ACVCLSSPKSCVFLKCGHVCSTECYRALPEPKKCPICROAITRVIPIYNS 352

RESULT 12
US-10-617-217A-73
Sequence 73, Application US/10617217A
Publication No. US20040081986A1
GENERAL INFORMATION:
APPLICANT: MATSUDA, Akio et al.
TITLE OF INVENTION: NF-KB ACTIVATING GENE
FILE REFERENCE: 1254-0229P
CURRENT APPLICATION NUMBER: US/10/617,217A
PRIOR FILING DATE: 2003-07-11
PRIOR APPLICATION NUMBER: JP 2000-402288
PRIOR FILING DATE: 2000-12-28
PRIOR APPLICATION NUMBER: JP 2001-088912
PRIOR FILING DATE: 2001-03-26
PRIOR APPLICATION NUMBER: JP 2001-254018
PRIOR FILING DATE: 2001-08-24
PRIOR APPLICATION NUMBER: US 60/258,315
PRIOR FILING DATE: 2000-12-28
PRIOR APPLICATION NUMBER: US 60/278,640
PRIOR FILING DATE: 2001-03-26
PRIOR APPLICATION NUMBER: US 60/314,385
PRIOR FILING DATE: 2001-08-24
NUMBER OF SEQ ID NOS: 224
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 73
LENGTH: 352
TYPE: PRT
ORGANISM: Homo sapiens
US-10-617-217A-73

Query Match 99.6%; Score 1824; DB 4; Length 352;
Best Local Similarity 99.7%; Pred. No. 4.9e-162;
Matches 351; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MESSGRPSLCQFILGTTSVVTAALYSYVRQKARVSGELKGAKKVLGEDLKSILSEAPG 60
DB 1 MESSGRPSLCQFILGTTSVVTAALYSYVRQKARVSGELKGAKKVLGEDLKSILSEAPG 60
QY 61 KCVPAVIEGAVRSYKETLNSQFVENCCKGVIGRLTLOEHKVMNRTTHLMDCKIHHOR 120
DB 61 KCVPAVIEGAVRSYKETLNSQFVENCCKGVIGRLTLOEHKVMNRTTHLMDCKIHHOR 120
QY 121 TMTVPDLVPHEDGDVAARVVKPLDSVDLGLETYKFKPFSIOSFTDVI GHYISGERPK 180
DB 121 TMTVPDLVPHEDGDVAARVVKPLDSVDLGLETYKFKPFSIOSFTDVI GHYISGERPK 180
QY 181 GIOETEMLVKVGATLTGVELVDNNSVRLQPPKQMGVYLLSQDFDLSLQROESSVRLM 240
DB 181 GIOETEMLVKVGATLTGVELVDNNSVRLQPPKQMGVYLLSQDFDLSLQROESSVRLM 240
QY 241 KVLALVFGPATCATLFFILRKQYLORQERLRLKQOEFOEHEAQLLSRAKPEDRESLKS 300
DB 241 KVLALVFGPATCATLFFILRKQYLORQERLRLKQOEFOEHEAQLLSRAKPEDRESLKS 300
QY 301 ACVCLSSPKSCVFLKCGHVCSTECYRALPEPKKCPICROAITRVIPIYNS 352
DB 301 ACVCLSSPKSCVFLKCGHVCSTECYRALPEPKKCPICROAITRVIPIYNS 352

RESULT 13
US-10-024-298A-73
Sequence 73, Application US/10024298A
Publication No. US20040214167A9
GENERAL INFORMATION:
APPLICANT: ASAH KASEI KABUSHIKI KAISHA
APPLICANT: AKIO MATSUDA
APPLICANT: GOICHI HONDA
APPLICANT: SHUKI MURAMATSU
APPLICANT: YUKIKO NAGANO
TITLE OF INVENTION: NF-KB Activating Gene
FILE REFERENCE: 1254-0191P
CURRENT APPLICATION NUMBER: US/10/024,298A
PRIOR FILING DATE: 2003-04-08
PRIOR APPLICATION NUMBER: 60/314,385
PRIOR FILING DATE: 2001-08-24
PRIOR APPLICATION NUMBER: 60/278,641
PRIOR FILING DATE: 2001-03-26
PRIOR APPLICATION NUMBER: 60/258,315
PRIOR FILING DATE: 2000-12-28
PRIOR APPLICATION NUMBER: JP254018/2001
PRIOR FILING DATE: 2001-08-24
PRIOR APPLICATION NUMBER: JP0088912/2001
PRIOR FILING DATE: 2001-03-26
PRIOR APPLICATION NUMBER: JP402288/2000
PRIOR FILING DATE: 2000-12-28
NUMBER OF SEQ ID NOS: 182
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 73
LENGTH: 352
TYPE: PRT
ORGANISM: Homo sapiens
US-10-024-298A-73

Query Match 99.6%; Score 1824; DB 4; Length 352;
Best Local Similarity 99.7%; Pred. No. 4.9e-162;
Matches 351; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MESSGRPSLCQFILGTTSVVTAALYSYVRQKARVSGELKGAKKVLGEDLKSILSEAPG 60
DB 1 MESSGRPSLCQFILGTTSVVTAALYSYVRQKARVSGELKGAKKVLGEDLKSILSEAPG 60
QY 61 KCVPAVIEGAVRSYKETLNSQFVENCCKGVIGRLTLOEHKVMNRTTHLMDCKIHHOR 120
DB 61 KCVPAVIEGAVRSYKETLNSQFVENCCKGVIGRLTLOEHKVMNRTTHLMDCKIHHOR 120

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Db      61 KCPVAVIEGAVRSVETLNSQFVENCCKVIOQLTQEHKVMWNTTTHLMDCKIIHOR 120
QY      121 TTTVPFDLVPHRDGDVAVRVLKPLDSVDLGHETVYKHPISIOSTVDYIGYISGERK 180
Db      121 TTTVPFDLVPHRDGDVAVRVLKPLDSVDLGHETVYKHPISIOSTVDYIGYISGERK 180
QY      181 GJOETEEMLKVGATLTGVELVDNNSVRLQPPKQMOYLLSSODPDSLQROESSVRLM 240
Db      181 GJOETEEMLKVGATLTGVELVDNNSVRLQPPKQMOYLLSSODPDSLQROESSVRLM 240
QY      241 KVLALVGFATCATLFFILRKQYLOEROERLRLKQMOEFQEHQAQLLSRAKPEDRESLKS 300
Db      241 KVLALVGFATCATLFFILRKQYLOEROERLRLKQMOEFQEHQAQLLSRAKPEDRESLKS 300
QY      301 ACVCLSSFKSCVFLGCGHVCSTECYRALPEPKKCPICROAITRVIPLYNS 352
Db      301 ACVCLSSFKSCVFLGCGHVCSTECYRALPEPKKCPICROAITRVIPLYNS 352

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RESULT 14

```

US-09-764-864-1262
; Sequence 1262, Application US/09764864
; Patent No. US20020132753A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PT223
; CURRENT APPLICATION NUMBER: US/09/764,864
; PRIOR FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 1792
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 1262
; LENGTH: 174
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (117)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-764-864-1262

```

```

Query Match          49.2%; Score 901; DB 3; Length 174;
Best Local Similarity 99.4%; Pred. No. 6e-76; Indels 0; Gaps 0;
Matches 173; Conservative 0; Mismatches 1;

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QY      179 PKGIOETEEMLKVGATLTGVELVDNNSVRLQPPKQMOYLLSSODPDSLQROESSVRLM 238
Db      1 PKGIOETEEMLKVGATLTGVELVDNNSVRLQPPKQMOYLLSSODPDSLQROESSVRLM 60
QY      239 LMKVTLALVGFATCATLFFILRKQYLOEROERLRLKQMOEFQEHQAQLLSRAKPEDRESL 298
Db      61 LMKVTLALVGFATCATLFFILRKQYLOEROERLRLKQMOEFQEHQAQLLSRAKPEDRESL 120
QY      299 KSACVCLSSFKSCVFLGCGHVCSTECYRALPEPKKCPICROAITRVIPLYNS 352
Db      121 KSACVCLSSFKSCVFLGCGHVCSTECYRALPEPKKCPICROAITRVIPLYNS 174

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RESULT 15

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US-10-264-237-2680
; Sequence 2680, Application US/10264237
; Publication No. US20040009491A1
; GENERAL INFORMATION:
; APPLICANT: Birse et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PA131P1
; CURRENT APPLICATION NUMBER: US/10/264,237
; PRIOR FILING DATE: 2002-10-04
; PRIOR APPLICATION NUMBER: PCT/US01/16450
; PRIOR FILING DATE: 2001-05-18
; PRIOR APPLICATION NUMBER: US 60/205,515
; PRIOR FILING DATE: 2000-05-19

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; NUMBER OF SEQ ID NOS: 2876
; SOFTWARE: Patentln Ver. 3.1
; SEQ ID NO 2680
; LENGTH: 165
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (108)
; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
US-10-264-237-2680

```

```

Query Match          46.6%; Score 854; DB 4; Length 165;
Best Local Similarity 99.4%; Pred. No. 1.4e-71;
Matches 164; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY      188 MLKVGATLTGVELVDNNSVRLQPPKQMOYLLSSODPDSLQROESSVRLMKVTLALVF 247
Db      1 MLKVGATLTGVELVDNNSVRLQPPKQMOYLLSSODPDSLQROESSVRLMKVTLALVF 60
QY      248 GPATCATLFFILRKQYLOEROERLRLKQMOEFQEHQAQLLSRAKPEDRESLKSACVCLLS 307
Db      61 GPATCATLFFILRKQYLOEROERLRLKQMOEFQEHQAQLLSRAKPEDRESLKSACVCLLS 120
QY      308 SFKSCVFLGCGHVCSTECYRALPEPKKCPICROAITRVIPLYNS 352
Db      121 SFKSCVFLGCGHVCSTECYRALPEPKKCPICROAITRVIPLYNS 165

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Search completed: February 24, 2006, 08:57:45
Job time : 165 secs

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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: February 24, 2006, 08:29:39 ; Search time 47 Seconds
(without alignments)
619.168 Million cell updates/sec

Title: US-09-978-360A-437

Perfect score: 1831
Sequence: 1 MESSGERPBLCOFILGTSV.....PKKPCICQATRVIPLYNS 352

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:
1: /cgn2_6/ptodata/1/1aa/5_COMB.pep:*
2: /cgn2_6/ptodata/1/1aa/6_COMB.pep:*
3: /cgn2_6/ptodata/1/1aa/8_COMB.pep:*
4: /cgn2_6/ptodata/1/1aa/PTUS_COMB.pep:*
5: /cgn2_6/ptodata/1/1aa/RE_COMB.pep:*
6: /cgn2_6/ptodata/1/1aa/backfilltest.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1831	100.0	352	US-09-599-360B-105	Sequence 105, App
2	445	24.3	91	US-08-905-223-421	Sequence 421, App
3	163	8.9	372	US-09-324-455-2	Sequence 2, App1
4	155.5	8.5	723	US-09-434-408-2	Sequence 2, App1
5	155.5	8.5	723	US-10-104-047-2572	Sequence 2572, App
6	151	8.2	350	US-09-270-767-58582	Sequence 58582, A
7	151	8.2	559	US-09-270-767-43239	Sequence 43239, A
8	144.5	7.9	438	PCT-US95-05922A-2	Sequence 2, App1
9	144.5	7.9	618	US-08-569-748-2	Sequence 2, App1
10	144.5	7.9	618	US-09-069-023-29	Sequence 29, App1
11	144.5	7.9	618	US-09-689-366-2	Sequence 2, App1
12	144.5	7.9	618	US-10-232-286-2	Sequence 2, App1
13	144.5	7.9	618	PCT-US96-12860-2	Sequence 2, App1
14	143.5	7.8	363	US-10-104-047-3425	Sequence 3425, App
15	138.5	7.6	618	US-08-511-485-8	Sequence 8, App1
16	138.5	7.6	618	US-09-212-971-8	Sequence 8, App1
17	138.5	7.6	618	US-08-800-929A-8	Sequence 8, App1
18	138.5	7.6	618	US-09-617-053A-8	Sequence 8, App1
19	138.5	7.6	618	US-09-201-936-8	Sequence 8, App1
20	138.5	7.6	618	US-09-011-356-8	Sequence 8, App1
21	138.5	7.6	618	US-09-672-717-223	Sequence 223, App
22	138.5	7.5	618	US-09-201-932-8	Sequence 8, App1
23	137.5	7.5	604	US-08-511-485-6	Sequence 6, App1
24	137.5	7.5	604	US-09-212-971-6	Sequence 6, App1
25	137.5	7.5	604	US-08-800-929A-6	Sequence 6, App1
26	137.5	7.5	604	US-09-617-053A-6	Sequence 6, App1
27	137.5	7.5	604	US-09-201-936-6	Sequence 6, App1

ALIGNMENTS

28	137.5	7.5	604	2	US-09-011-356-6	Sequence 6, App1
29	137.5	7.5	604	2	US-09-672-717-221	Sequence 221, App
30	137.5	7.5	604	2	US-09-201-932-6	Sequence 6, App1
31	136.5	7.5	602	2	US-09-201-936-40	Sequence 40, App1
32	136.5	7.5	602	2	US-09-011-356-40	Sequence 40, App1
33	136.5	7.5	602	2	US-09-672-717-227	Sequence 227, App
34	136.5	7.5	602	2	US-09-201-932-40	Sequence 40, App1
35	133.5	7.2	612	2	US-08-569-749-14	Sequence 14, App1
36	133.5	7.2	612	2	US-09-689-366-14	Sequence 14, App1
37	132.5	7.2	612	2	US-10-232-286-14	Sequence 14, App1
38	132.5	7.2	612	4	PCT-US96-12860-14	Sequence 14, App1
39	128.5	7.0	600	2	US-09-212-971-12	Sequence 12, App1
40	128.5	7.0	600	2	US-08-800-929A-12	Sequence 12, App1
41	128.5	7.0	600	2	US-09-617-053A-12	Sequence 12, App1
42	128.5	7.0	612	2	US-09-212-971-14	Sequence 14, App1
43	128.5	7.0	612	2	US-08-800-929A-14	Sequence 14, App1
44	128.5	7.0	612	2	US-09-617-053A-14	Sequence 14, App1
45	127.5	7.0	591	2	US-09-201-936-42	Sequence 42, App1

```

RESULT 1
US-09-599-360B-105
; Sequence 105, Application US/09599360B
; Patent No. 6548633
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Bouguetier, L.
; TITLE OF INVENTION: Complementary DNA's Encoding Proteins with Signal Peptides
; FILE REFERENCE: GENSER.050C93
; CURRENT APPLICATION NUMBER: US/09/599,360B
; PRIOR FILING DATE: 2000-06-21
; PRIOR APPLICATION NUMBER: 60/113,686
; PRIOR FILING DATE: 1998-12-22
; PRIOR APPLICATION NUMBER: 60/141,032
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: 09/469,099
; PRIOR FILING DATE: 1999-12-21
; NUMBER OF SEQ ID NOS: 123
; SOFTWARE: Patent.pm
; SEQ ID NO 105
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: ~23..-1
US-09-599-360B-105
Query Match 100.0%; Score 1831; DB 2; Length 352;
Best Local Similarity 100.0%; Pred. No. 1.7e-192;
Matches 352; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
1 MESSGERPBLCOFILGTSVVTALYSYRQKARVSGELKAKKHLSEDLKSLISEAPG 60
1 MESSGERPBLCOFILGTSVVTALYSYRQKARVSGELKAKKHLSEDLKSLISEAPG 60
1 MESSGERPBLCOFILGTSVVTALYSYRQKARVSGELKAKKHLSEDLKSLISEAPG 60
KCVPAVLEGAVRSVKTETNSQFVENCNGVIOPLTLOSHKVMWNTTILMNDCKIHOR 120
KCVPAVLEGAVRSVKTETNSQFVENCNGVIOPLTLOSHKVMWNTTILMNDCKIHOR 120
KCVPAVLEGAVRSVKTETNSQFVENCNGVIOPLTLOSHKVMWNTTILMNDCKIHOR 120
TNTVFPDLVPHEDGVAVRVLKPLDSVDLGLFTYEFKHPISIOFTDVIIGHYISGERPK 180
TNTVFPDLVPHEDGVAVRVLKPLDSVDLGLFTYEFKHPISIOFTDVIIGHYISGERPK 180
TNTVFPDLVPHEDGVAVRVLKPLDSVDLGLFTYEFKHPISIOFTDVIIGHYISGERPK 180
TNTVFPDLVPHEDGVAVRVLKPLDSVDLGLFTYEFKHPISIOFTDVIIGHYISGERPK 180
GIQTEBEMKATGATITGELVLDNNSVRLQPPKQMGYYLSSODFSLLORESSVFLW 240
GIQTEBEMKATGATITGELVLDNNSVRLQPPKQMGYYLSSODFSLLORESSVFLW 240
GIQTEBEMKATGATITGELVLDNNSVRLQPPKQMGYYLSSODFSLLORESSVFLW 240
GIQTEBEMKATGATITGELVLDNNSVRLQPPKQMGYYLSSODFSLLORESSVFLW 240
KVALVFGFATCATLFFILRKQVLRQERLRLLKQWQEFQEHQAQLLSRAKPEDRESLKS 300

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Db 241 KVALIVEGPAATCATLFFILRKQYQROERLRLKQMOEFQEHRAQLLSRAKPEDRESLKS 300
QY 301 ACVCCLASSFSCVLECGHVCSTECYRALPEPKKPCICQATRVIPLYNS 352
Db 301 ACVCCLASSFSCVLECGHVCSTECYRALPEPKKPCICQATRVIPLYNS 352

RESULT 2
US-08-905-223-421
; Sequence 421, Application US/08905223
; Patent No. 6222029
; GENERAL INFORMATION:
; APPLICANT: Edwards, Jean-Baptiste D.
; APPLICANT: Duclert, Americ
; APPLICANT: Lacroix, Bruno
; TITLE OF INVENTION: 5' ESTS FOR SECRETED PROTEINS
; NUMBER OF SEQUENCES: 503
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Knobbe, Martens, Olson & Bear
; STREET: 501 West Broadway
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92101-3505
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Win95
; SOFTWARE: Word
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/905,223
; FILING DATE:
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Israelien, Ned A.
; REGISTRATION NUMBER: 29,655
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 235-8550
; TELEFAX: (619) 235-0176
; INFORMATION FOR SEQ ID NO: 421:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 91 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: LINEAR
; MOLECULE TYPE: PROTEIN
; ORIGINAL SOURCE:
; ORGANISM: Homo Sapiens
; TISSUE TYPE: Brain
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: -23...-1
; IDENTIFICATION METHOD: Von Heijne matrix
; OTHER INFORMATION: score 4.4
; OTHER INFORMATION: seq 0FILLGTSVTA/AL
US-08-905-223-421

Query Match 24.3%; Score 445; DB 2; Length 91;
Best Local Similarity 98.9%; Pred. No. 5.8e-41;
Matches 89; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 MESGGSPSLCQFILLGTSVTAALYSVYRKARVSOELKGAKVHLGDLKSLSEAG 60
Db 1 MESGGSPSLCQFILLGTSVTAALYSVYRKARVSOELKGAKVHLGDLKSLSEAG 60
QY 61 KCPYAVITGAVSVETLNSQVENCXGY 90
Db 61 KCPYAVITGAVSVETLNSQVENCXGY 90

RESULT 3
US-09-324-455-2

; Sequence 2, Application US/09324455
; Patent No. 6326481
; GENERAL INFORMATION:
; APPLICANT: yowe, David
; TITLE OF INVENTION: NOVEL MOLECULES OF THE AIP-RELATED
; TITLE OF INVENTION: PROTEIN FAMILY AND USES THEREOF
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: FastSeq for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/324,455
; FILING DATE: 02-JUN-1999
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/087,761
; FILING DATE: 02-JUN-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: WeikieJom, Ph.D., Anita L.
; REGISTRATION NUMBER: 35,283
; REFERENCE/DOCKET NUMBER: 07334/069001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/542-5070
; TELEFAX: 617/542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 372 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-324-455-2

Query Match 8.9%; Score 163; DB 2; Length 372;
Best Local Similarity 30.1%; Pred. No. 6.2e-09;
Matches 40; Conservative 29; Mismatches 48; Indels 16; Gaps 5;
QY 222 SQDPDSLQROESSVR-LMKVLAIVF-GRATCATLFFILRKQYQROERLRLKQMOEF 279
Db 254 SLSDLSIDVDYGVMSVRLKEILARNFVYSGCEKMWLVER-----VNLRYKEN 303
QY 280 OEHAQQLLSRAKPEDRESLKSACVYCVFLECGHVCSTECYRALPEPKKPCIC 339
Db 304 EBNQSYGERLQDDEE-DSLICRIMDAVIDCVLBCGHVVTCTKCGKRWSE---CPTC 359
QY 340 RQATRVIPLYNS 352
Db 360 RQYVRAVHVFES 372

RESULT 4
US-09-434-408-2
; Sequence 2, Application US/09434408
; Patent No. 6440697
; GENERAL INFORMATION:
; APPLICANT: Domenick
; APPLICANT: Grossmann, Angelika
; TITLE OF INVENTION: RING FINGER PROTEIN ZAPOR3
; FILE REFERENCE: 98-41
; CURRENT APPLICATION NUMBER: US/09/434,408
; CURRENT FILING DATE: 1999-11-04
; EARLIER APPLICATION NUMBER: US 60/108,258
; EARLIER FILING DATE: 1998-11-12
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 2
LENGTH: 723
TYPE: PRT
ORGANISM: Homo sapiens
US-09-434-408-2

Query Match 8.5%; Score 155.5; DB 2; Length 723;
Best Local Similarity 34.3%; Pred. No. 1.2e-07;
Matches 37; Conservative 16; Mismatches 38; Indels 17; Gaps 3;

QY 259 LKQYLRQERLRLKQOEERF-----QEHLAQLLSRAKPEDRESLSKACV 304
DB 618 LQHEILRRVQELDLARIQPELKPMPGEVVTPTAQEPESVRSPAPPALELVQASECV 677
QY 305 CLASSFKCVPLECGHVCSTECYRALPEPKKCPICROAITRVIPLYNS 352
DB 678 CLERBAQMIPLNGHVCVCCQCCQCPPL---RTCPICRODIAQRLRIYHS 722

RESULT 5
US-10-104-047-2572
Sequence 2572; Application US/10104047
Patent No. 6943241
GENERAL INFORMATION:
APPLICANT: HELIX RESEARCH INSTITUTE
TITLE OF INVENTION: No. 6943241e1 full length cDNA
FILE REFERENCE: H1-A0105
CURRENT APPLICATION NUMBER: US/10/104,047
CURRENT FILING DATE: 2002-03-25
PRIOR APPLICATION NUMBER:
NUMBER OF SEQ ID NOS: 4096
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 2572
LENGTH: 723
TYPE: PRT
ORGANISM: Homo sapiens
US-10-104-047-2572

Query Match 8.5%; Score 155.5; DB 2; Length 723;
Best Local Similarity 34.3%; Pred. No. 1.2e-07;
Matches 37; Conservative 16; Mismatches 38; Indels 17; Gaps 3;

QY 259 LKQYLRQERLRLKQOEERF-----QEHLAQLLSRAKPEDRESLSKACV 304
DB 618 LQHEILRRVQELDLARIQPELKPMPGEVVTPTAQEPESVRSPAPPALELVQASECV 677
QY 305 CLASSFKCVPLECGHVCSTECYRALPEPKKCPICROAITRVIPLYNS 352
DB 678 CLERBAQMIPLNGHVCVCCQCCQCPPL---RTCPICRODIAQRLRIYHS 722

RESULT 6
US-09-270-767-58582
Sequence 58582; Application US/09270767
Patent No. 6703491
GENERAL INFORMATION:
APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
FILE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 58582
LENGTH: 350
TYPE: PRT
ORGANISM: Drosophila melanogaster
FEATURE:
OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-58582

Query Match 8.2%; Score 151; DB 2; Length 350;

Best Local Similarity 31.5%; Pred. No. 1.2e-07;
Matches 34; Conservative 18; Mismatches 34; Indels 22; Gaps 3;

QY 264 LQROERLRLKQOEERFQEH-----EAQLLSRAK-----PEDRESLSKACV 304
DB 102 LKDEGLTVQKQKEVLMHRYDYKGCCEKQELDRVSRMTKMECPAWEKLADELCKI 161
QY 305 CLASSFKCVPLECGHVCSTECYRALPEPKKCPICROAITRVIPLYNS 352
DB 162 CMDAPIECVPLECGHVMATCTSCGVKLVN---CPICROYIVRVVFFRA 206

RESULT 7
US-09-270-767-43239
Sequence 43239; Application US/09270767
Patent No. 6703491
GENERAL INFORMATION:
APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
FILE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 43239
LENGTH: 559
TYPE: PRT
ORGANISM: Drosophila melanogaster
FEATURE:
OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-43239

Query Match 8.2%; Score 151; DB 2; Length 559;
Best Local Similarity 31.5%; Pred. No. 2.5e-07;
Matches 34; Conservative 18; Mismatches 34; Indels 22; Gaps 3;

QY 264 LQROERLRLKQOEERFQEH-----EAQLLSRAK-----PEDRESLSKACV 304
DB 311 LKDEGLTVQKQKEVLMHRYDYKGCCEKQELDRVSRMTKMECPAWEKLADELCKI 370
QY 305 CLASSFKCVPLECGHVCSTECYRALPEPKKCPICROAITRVIPLYNS 352
DB 371 CMDAPIECVPLECGHVMATCTSCGVKLVN---CPICROYIVRVVFFRA 415

RESULT 8
PCT-US95-05922A-2
Sequence 2; Application PC/TUS9505922A
GENERAL INFORMATION:
APPLICANT: HE, ET. AL.
TITLE OF INVENTION: Human Inhibitor of Apoptosis Gene 1
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
STREET: 6 BECKER FARM ROAD
CITY: ROSELAND
STATE: NEW JERSEY
COUNTRY: USA
ZIP: 07068
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH DISKETTE
COMPUTER: IBM PS/2
OPERATING SYSTEM: MS-DOS
SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/05922A
FILING DATE: 11 MAY 1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:

NAME: FERRARO, GREGORY D.
 REGISTRATION NUMBER: 36,134
 TELEPHONE: (415) 781-1989
 TELEFAX: (415) 398-3249
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 201-994-1700
 TELEFAX: 201-994-1744
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 438 AMINO ACIDS
 TYPE: AMINO ACID
 STRANDEDNESS:
 TOPOLOGY: LINEAR
 MOLECULE TYPE: PROTEIN
 PCT-US95-05922A-2

Query Match
 Best Local Similarity 21.9%; Score 144.5; DB 4; Length 438;
 Matches 68; Conservative 50; Mismatches 118; Indels 75; Gaps 13;

QY 82 QPVENCQVIGRLTLQEHKVMNRTHLMNDCSKIHQRTNTVPFDLVPHEDGVAVRV 141
 DB 163 EFVDEIQGRYPHLL--EQLISTSDTGTGENADPPIH-----FGPGESSSEDVMM 211
 QY 142 LKPL--DSVDLGL-----ETVYEKHPISQSF--TDVIGHYISGERPKGIOE---TE 186
 DB 212 NTPVVKSALEMGFNRDLVKQTVQSKILTTGENYKTVNDIVSALINADEKREKEKQAE 271
 QY 187 EMLKVGATLTGVEL-----VLDN---NSVRLQPP---KQGMQYILSSQD--FD 227
 DB 272 EWASDLSLIRKRMALFQQLTCVLPILDNLKAVINKQEHDIKQKTQIPLOARELID 331
 QY 228 SLLOQESSVRLMKYALVFGFATCATLFFILRKQYLQROE-----RLRKQMOEFQOE 281
 DB 332 TLVKGNAANIFKNCLEIDSTLYKNLFVDKNMKYIPTEEDVSGLSLEQRLRQOE--- 388
 QY 282 HEAQLSRAPKEDRESLSACVCLSFKSCVFLGCHGVCSTCEYALPEPKKPCICQ 341
 DB 389 -----RTCKVCMDKEVSVPFPGHLVVCQEC--APSLRKCPCICG 427
 QY 342 AITRVIPLYNS 352
 DB 428 IIKGTVRTPLS 438

RESULT 9
 US-08-569-749-2
 Sequence 2, Application US/08569749
 Patent No. 6187557
 GENERAL INFORMATION:
 APPLICANT: Rothe, Mike
 APPLICANT: Goeddel, David V
 TITLE OF INVENTION: INHIBITORS OF APOPTOSIS
 NUMBER OF SEQUENCES: 14
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: FLEHR, HOHBACH, TEST, ALBRITTON & HERBERT
 STREET: 4 Embarcadero Center, Suite 3400
 CITY: San Francisco
 STATE: California
 COUNTRY: USA
 ZIP: 94111
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/569,749
 FILING DATE:
 CLASSIFICATION: 514
 ATTORNEY/AGENT INFORMATION:
 NAME: Brezner, David J.
 REGISTRATION NUMBER: 24,774
 REFERENCE/DOCKET NUMBER: A-62464/DJB

TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 781-1989
 TELEFAX: (415) 398-3249
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 618 AMINO ACIDS
 TYPE: AMINO ACID
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-569-749-2

Query Match
 Best Local Similarity 21.9%; Score 144.5; DB 2; Length 618;
 Matches 68; Conservative 50; Mismatches 118; Indels 75; Gaps 13;

QY 82 QPVENCQVIGRLTLQEHKVMNRTHLMNDCSKIHQRTNTVPFDLVPHEDGVAVRV 141
 DB 343 EFVDEIQGRYPHLL--EQLISTSDTGTGENADPPIH-----FGPGESSSEDVMM 391
 QY 142 LKPL--DSVDLGL-----ETVYEKHPISQSF--TDVIGHYISGERPKGIOE---TE 186
 DB 392 NTPVVKSALEMGFNRDLVKQTVQSKILTTGENYKTVNDIVSALINADEKREKEKQAE 451
 QY 187 EMLKVGATLTGVEL-----VLDN---NSVRLQPP---KQGMQYILSSQD--FD 227
 DB 452 EWASDLSLIRKRMALFQQLTCVLPILDNLKAVINKQEHDIKQKTQIPLOARELID 511
 QY 228 SLLOQESSVRLMKYALVFGFATCATLFFILRKQYLQROE-----RLRKQMOEFQOE 281
 DB 512 TLVKGNAANIFKNCLEIDSTLYKNLFVDKNMKYIPTEEDVSGLSLEQRLRQOE--- 568
 QY 282 HEAQLSRAPKEDRESLSACVCLSFKSCVFLGCHGVCSTCEYALPEPKKPCICQ 341
 DB 569 -----RTCKVCMDKEVSVPFPGHLVVCQEC--APSLRKCPCICG 607
 QY 342 AITRVIPLYNS 352
 DB 608 IIKGTVRTPLS 618

RESULT 10
 US-09-069-023-29
 Sequence 29, Application US/09069023A
 Patent No. 6348573
 GENERAL INFORMATION:
 APPLICANT: Nunez, Gabriel
 APPLICANT: Inohara, Naohiro
 APPLICANT: Koseki, Takeyoshi
 TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR IDENTIFYING APOPTOSIS
 FILE REFERENCE: UM-03333
 CURRENT APPLICATION NUMBER: US/09/069,023A
 CURRENT FILING DATE: 1998-04-27
 NUMBER OF SEQ ID NOS: 38
 SOFTWARE: Patentin Ver. 2.0
 SEQ ID NO 29
 LENGTH: 618
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-09-069-023-29

Query Match
 Best Local Similarity 21.9%; Score 144.5; DB 2; Length 618;
 Matches 68; Conservative 50; Mismatches 118; Indels 75; Gaps 13;

QY 82 QPVENCQVIGRLTLQEHKVMNRTHLMNDCSKIHQRTNTVPFDLVPHEDGVAVRV 141
 DB 343 EFVDEIQGRYPHLL--EQLISTSDTGTGENADPPIH-----FGPGESSSEDVMM 391
 QY 142 LKPL--DSVDLGL-----ETVYEKHPISQSF--TDVIGHYISGERPKGIOE---TE 186
 DB 392 NTPVVKSALEMGFNRDLVKQTVQSKILTTGENYKTVNDIVSALINADEKREKEKQAE 451

QY 187 EMLKATLTGVGEL-----VLDN-----NSVRLQPP---KQGMYYLSSOD--FD 227
DB 452 EMASDLSLRKNRRAALFQOULTCVLPIDNLLKANVINKQEHDIKQTKQIPLQARELID 511
QY 228 SLROESSVRLMKYALVFGFATCATLFFILRKOYLOQOE-----RLRLKQMOEERFOE 281
DB 512 TLIVGNAANAFKNCLEIDSTLYKNLFVDKMKYIPTEDVSGLSLEQJRLQOE--- 568
QY 282 HEAQLLSRAKPBDRSLKACVVCISSEFKSVFLECGHVCSTCEYRALPEPKCPIRQ 341
DB 569 -----RTCKVCMDKEVSVVFIPCGHLVVCQEC---APSLRKCPICRG 607
QY 342 AITRVIPLVNS 352
DB 608 IIKGTVRTFLS 618

RESULT 11

US-09-689-366-2
Sequence 2, Application US/09689366
Patent No. 6821736
GENERAL INFORMATION:
APPLICANT: Rothe, Mike
Goedel, David V
TITLE OF INVENTION: INHIBITORS OF APOPTOSIS
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: FLEHR, HOHBACH, TEST, ALBRITTON & HERBERT
STREET: 4 Embarcadero Center, Suite 3400
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/689,366
FILING DATE: 10-Dec-2000
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/569,749
FILING DATE: 08-Dec-1995
ATTORNEY/AGENT INFORMATION:
NAME: Brezner, David J.
REGISTRATION NUMBER: 24,774
REFERENCE/DOCKET NUMBER: A-62464/DJB
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415)781-1989
TELEFAX: (415)398-3249
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 618 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-689-366-2

Query Match 7.9%; Score 144.5; DB 2; Length 618;
Best Local Similarity 21.9%; Pred. No. 1.5e-06;
Matches 68; Conservative 50; Mismatches 118; Indels 75; Gaps 13;
QY 82 QVENVCKGVIOQLTLOEHKMMNRTHLMNDCKSIHQRTNTVPFPLVPHEDGVAVAV 141
DB 343 EFDVDEIQGRYPRLT--EQLLSTSDTGTGENADPPIIH-----FGGSSSSSDAVMM 391
QY 142 LKPL--DSVDLGL-----ETVYEKPHPSIQSF---TDVIGHYISGERPKGIOE---TE 186

DB 392 NTPVKSALENGFNRLDVKQTVOSKILTTGNTYKTVNDIVSALINADEKREKEKQAE 451
QY 187 EMLKATLTGVGEL-----VLDN-----NSVRLQPP---KQGMYYLSSOD--FD 227
DB 452 EMASDLSLRKNRRAALFQOULTCVLPIDNLLKANVINKQEHDIKQTKQIPLQARELID 511
QY 228 SLROESSVRLMKYALVFGFATCATLFFILRKOYLOQOE-----RLRLKQMOEERFOE 281
DB 512 TLIVGNAANAFKNCLEIDSTLYKNLFVDKMKYIPTEDVSGLSLEQJRLQOE--- 568
QY 282 HEAQLLSRAKPBDRSLKACVVCISSEFKSVFLECGHVCSTCEYRALPEPKCPIRQ 341
DB 569 -----RTCKVCMDKEVSVVFIPCGHLVVCQEC---APSLRKCPICRG 607
QY 342 AITRVIPLVNS 352
DB 608 IIKGTVRTFLS 618

RESULT 12

US-10-232-286-2
Sequence 2, Application US/10232286
Patent No. 6855815
GENERAL INFORMATION:
APPLICANT: Rothe, Mike
Goedel, David V
TITLE OF INVENTION: INHIBITORS OF APOPTOSIS
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: FLEHR, HOHBACH, TEST, ALBRITTON & HERBERT
STREET: 4 Embarcadero Center, Suite 3400
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/232,286
FILING DATE: 30-Aug-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/569,749
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Brezner, David J.
REGISTRATION NUMBER: 24,774
REFERENCE/DOCKET NUMBER: A-62464/DJB
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415)781-1989
TELEFAX: (415)398-3249
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 618 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-232-286-2

Query Match 7.9%; Score 144.5; DB 2; Length 618;
Best Local Similarity 21.9%; Pred. No. 1.5e-06;
Matches 68; Conservative 50; Mismatches 118; Indels 75; Gaps 13;
QY 82 QVENVCKGVIOQLTLOEHKMMNRTHLMNDCKSIHQRTNTVPFPLVPHEDGVAVAV 141
DB 343 EFDVDEIQGRYPRLT--EQLLSTSDTGTGENADPPIIH-----FGGSSSSSDAVMM 391
QY 142 LKPL--DSVDLGL-----ETVYEKPHPSIQSF---TDVIGHYISGERPKGIOE---TE 186

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Db      392 NTFVVKASLEMGFRDLVKTQVQSKILITGENTVWDIVSALINAEDEKREBEKEKQAE
Qy      187 EMLKVGATLTGVGEL-----VLDN-----NSVRLQPP---KQGMQYLLSSQD-FD 227
Db      452 EMASDDLSTLRKNRMALFQQLTCVLPILDNLLKANVINKQEHDIKQKQIPLOARELID 511
Qy      228 SLQROESSVRLMKVLALVFGATCATLFFILRKQYLOQOE-----RLRKQOEERFOE 281
Db      512 TLIVKGNMAANIFKQCLKEIDSTLYKNLFVDKRMKYIPTEDVSGLSLEQLRLQOE--- 568
Qy      282 HEAQLSRAKPEDRESLSKACVCLSSPKSCVFLGCHVCSCTECYRALPEPKKPCICRQ 341
Db      569 -----RTCKVCMDEKESVVFICGHLVVCQEC---APSLRKPCICRG 607
Qy      342 AITRVIPLYNS 352
Db      608 IIKGTVRTPLS 618

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RESULT 13

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PCT-US96-12860-2
; Sequence 2, Application PC/TUS9612860
; GENERAL INFORMATION:
; APPLICANT: TULARIK, INC.
; TITLE OF INVENTION: INHIBITORS OF APOPTOSIS
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FLEHR, HOHBACH, TEST, ALBRITTON & HERBERT
; STREET: 4 Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/12860
; FILING DATE: 06 AUG 1996
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: U.S. Serial Nos. 08/512,946 & 08/569,749
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Breznet, David J.
; REGISTRATION NUMBER: 24,774
; REFERENCE/DOCKET NUMBER: A-62464/DJB
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415)781-1989
; TELEFAX: (415)398-3249
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 618 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; PCT-US96-12860-2

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Query Match      7.8%; Score 144.5; DB 4; Length 618;
Best Local Similarity 21.9%; Pred. No. 1.5e-06;
Matches 68; Conservative 50; Mismatches 118; Indels 75; Gaps 13;

Qy      82 OFVENCKGYQRTLTQEHKVMNRTHLWNNDSKILHQRNTVPRDLYVHEGCVAAKRV 141
Db      343 EFDDELQSGKYPHL--EQILISTDITGEENADPPH-----FGGESSSDDAVMM 391
Qy      142 LKPL--DSVDLGI-----ETVVEKFPISIQSF--TDVIGHYISGERPKGIOE---TE 186
Db      392 NTFVVKASLEMGFRDLVKTQVQSKILITGENTVWDIVSALINAEDEKREBEKEKQAE 451

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Qy      187 EMLKVGATLTGVGEL-----VLDN-----NSVRLQPP---KQGMQYLLSSQD-FD 227
Db      452 EMASDDLSTLRKNRMALFQQLTCVLPILDNLLKANVINKQEHDIKQKQIPLOARELID 511
Qy      228 SLQROESSVRLMKVLALVFGATCATLFFILRKQYLOQOE-----RLRKQOEERFOE 281
Db      512 TLIVKGNMAANIFKQCLKEIDSTLYKNLFVDKRMKYIPTEDVSGLSLEQLRLQOE--- 568
Qy      282 HEAQLSRAKPEDRESLSKACVCLSSPKSCVFLGCHVCSCTECYRALPEPKKPCICRQ 341
Db      569 -----RTCKVCMDEKESVVFICGHLVVCQEC---APSLRKPCICRG 607
Qy      342 AITRVIPLYNS 352
Db      608 IIKGTVRTPLS 618

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RESULT 14

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US-10-104-047-3425
; Sequence 3425, Application US/10104047
; Patent No. 6943241
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: No. 6943241e1 full length cDNA
; FILE REFERENCE: H1-A0105
; CURRENT APPLICATION NUMBER: US/10/104,047
; PRIOR FILING DATE: 2002-03-25
; PRIOR APPLICATION NUMBER:
; NUMBER OF SEQ ID NOS: 4096
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 3425
; LENGTH: 363
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-104-047-3425

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Query Match      7.8%; Score 143.5; DB 2; Length 363;
Best Local Similarity 30.1%; Pred. No. 8.3e-07;
Matches 41; Conservative 28; Mismatches 40; Indels 27; Gaps 7;

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Qy      224 QDFDSLQROESSVRLMKVLALVFGATCATLFFILRKQYLOQOEERLRLKQOEERFOE 281
Db      248 EDIBELTVRQ-----LKEILARNPVNYKGCCEKEELM-----ERYTRLKQKQIQ- 293
Qy      282 HEAQLSRAKPEDRESLSKSA-----CVVCLSSPKSCVFLGCHVCSCTECYRALPEPKKC 336
Db      294 --HIVSGABDONGGAVSGGLEENLCKICMDSPIDCVLLEGHNVTCCKGKRMNE---C 347
Qy      337 PICROAIRVPIPLVNS 352
Db      348 PICROYIRAVHVFNS 363

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RESULT 15

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US-08-511-485-8
; Sequence 8, Application US/08511485
; Patent No. 5919912
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: Mackenzie, Alexander E.
; TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY PRIMERS,
; TITLE OF INVENTION: PROBES, AND DETECTION METHODS
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110-2804

```

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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/511,485
FILING DATE: 04-AUG-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 07540/002001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 618 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: both
MOLECULE TYPE: protein
US-08-511-485-8

```

```

Query Match      7.6%; Score 138.5; DB 1; Length 618;
Best Local Similarity 21.5%; Pred. No. 7e-06;
Matches 67; Conservative 50; Mismatches 119; Indels 75; Gaps 13;

QY 82 QVENCKGVIOQLTQEHKVMNRTTHLNDCKIITHORTNVPFDLVPHEDGVDAVRV 141
DB 343 EYVDIQRYPHLL--EQLISTSDTTGEENADPPIIH-----FGPGESSSEDVAVM 391
QY 142 LKPL--DSVDLGL-----EYVEKPHPSIQSF---TDVIGYISGERPKGIOE---TE 186
DB 392 NTPVVKSLKEMGFNDLVKQTVLSKILTTGENYKTVNDIVSALNADEKREBEKQAE 451
QY 187 EMLKVGATILTVGEL-----VLDN---NSVRLQPP--KQMQYTLSSOD--FD 227
DB 452 EWAASDLSLRKRMALFQQLTCVLPILDNLKANVINKEHDIIKQKTQIPLQARBLID 511
QY 228 SLLOQESSVRLMKVLALVGFATCATLFFILRKQYLORE-----RLRLKQOEPEQE 281
DB 512 TIWVGNAANIFKQCKLEIDSTLYKNLFPDKMKKITPTEDVSGLSLEQLRLQBE--- 568
QY 282 HEAQLLSRAKPEDRESLSKACVCLSSFKSCVFLBCGHVCSCTECYRALPEPKCPICRO 341
DB 569 -----RTCKVCMDKEVSVFIFQGHILVQCQC---APSLRKCPICKG 607
QY 342 AITRVIPLYNS 352
DB 608 IIKGTVRTFLS 618

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Search completed: February 24, 2006, 08:31:00
Job time : 48 secs

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OM protein - protein search, using sw model

Run on: February 24, 2006, 08:22:24 ; Search time 230 Seconds
(without alignments)
1079.765 Million cell updates/sec

Title: US-09-978-360A-437

Perfect score: 1831

Sequence: 1 MESGRPSLCCFILLGTTSV.....PKKCPICQALTRVPLXNS 352

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Uniprot 05.80:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1831	100.0	352	2	0969V5_HUMAN
2	1824	99.6	352	2	072431_HUMAN
3	1818	99.3	352	2	0949B5_HUMAN
4	1815	99.1	352	2	0479G8_MACACA
5	1673	91.4	352	2	08VCM5_MOUSE
6	1672	91.3	352	2	08BHF2_MOUSE
7	1667	91.0	352	2	09DCV9_MOUSE
8	1277.5	69.8	353	2	06NTT6_XENILA
9	1145	62.5	352	2	0456B4_TETNG
10	776	42.4	341	2	05M7X9_BRARE
11	442.5	24.2	338	2	09VZJ9_DROME
12	436	23.8	339	2	0706A1_ANGOA
13	431.5	23.6	206	2	04RV85_TETNG
14	391.5	21.4	283	2	06PBA9_BRARE
15	384.5	21.0	221	2	06AX71_XENILA
16	301	16.4	343	2	08L7N4_ARATH
17	267.5	14.6	338	2	094HV7_ARATH
18	266	14.5	341	2	09LO59_ARATH
19	230.5	12.6	237	2	09SLU0_ARATH
20	201	11.0	383	2	09STH3_ARATH
21	192	10.5	383	2	04VVC9_MEDTR
22	166	9.1	376	2	099KR6_MOUSE
23	166	9.1	381	2	08CIP0_RAT
24	166	9.1	381	2	06AYH3_RAT
25	166	9.1	402	2	070VP2_GIALA
26	165.5	9.0	355	2	04V818_XENILA
27	165.5	9.0	363	2	04V919_BRARE
28	164.5	9.0	262	2	05DC20_SCHUA
29	164.5	9.0	375	2	05E9J6_BOVIN
30	164.5	9.0	382	2	06GNI9_XENILA
31	164	9.0	372	2	09HEW8_HUMAN

32	163	8.9	372	2	0969K3_HUMAN
33	163	8.9	372	2	05NV17_PONPY
34	163	8.9	372	2	05NVCT_PONPY
35	163	8.9	373	2	08NG47_HUMAN
36	163	8.9	373	2	05R509_PONPY
37	162.5	8.9	727	1	LRSM1_MOUSE
38	160.5	8.8	257	2	0516W9_ENTHI
39	156	8.5	628	2	08UWD2_BRARE
40	156	8.5	647	2	0770K2_BRARE
41	156	8.5	654	2	06ZM93_BRARE
42	156	8.5	699	2	095TH2_DROME
43	155.5	8.5	333	2	04RXJ0_TETNG
44	155.5	8.5	723	1	LRSM1_HUMAN
45	154.5	8.4	329	2	05BL61_XENTR

ALIGNMENTS

RESULT 1
0969V5_HUMAN
ID 0969V5; HUMAN PRELIMINARY; PRT; 352 AA.
AC 0969V5;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 13-SEP-2005 (TREMBlrel. 31, Last annotation update)
DE Hypothetical protein Clorf166 (Hypothetical protein FLJ12875) (Novel protein) (Hypothetical protein DKFZp762M0911).
GN Name=Clorf166; Synonyms=DKFZp762M0911, FLJ12875, RP11-401M16.2;
GN ORFNames=RP11-401M16.2-001;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
OC Homo.
OC NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Brain, and Skin;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Staciecon M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein W.J., Ueda T.B., Toshitoki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton B., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A.C., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield V.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Skin;
RG NIH MGC Project;
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Brain;
RL Strausberg R.;
RN Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
RP NUCLEOTIDE SEQUENCE.
RL Kimberley A.;
RN Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.

[5]
 RN NUCLEOTIDE SEQUENCE.
 RC TISSUE=Melanoma;
 RG The German cDNA Consortium;
 RA Blum H., Bauerbachs S., Mewes H.W., Weil B., Amid C., Oeanger A.,
 RA Fobo G., Han M., Wilmann S.;
 RL Submitted (JAN-2005) to the EMBL/GenBank/DBJ databases.
 DR EMBL: BC014010; AAH14010.1; -; mRNA.
 DR EMBL: BC010101; AAH10101.1; -; mRNA.
 DR EMBL: AL381357; CAH73470.1; -; Genomc.-DNA.
 DR EMBL: AL833889; CAD38745.1; -; mRNA.
 DR KJ0000000090432; Homo sapiens.
 DR GO: GO:0004871; F: signal transducer activity; IMP.
 DR GO: GO:0043123; P: positive regulation of I-kappa kinase/NF-k. .; IMP.
 DR InterPro: IPR001841; Znf_RING.
 DR SMART: SM00184; RING_1.
 DR PROSITE: PS50089; ZF_RING_2; 1.
 DR Hypothetical protein; Metal-binding; Zinc; Zinc-finger.
 KM Hypothetical protein; Metal-binding; Zinc; Zinc-finger.
 SQ SEQUENCE 352 AA; 39800 MW; 6EF2B8BCE1801F CRC64;

Query Match 100.0%; Score 1831; DB 2; Length 352;
 Best Local Similarity 100.0%; Pred. No. 3.3e-129; Indels 0; Gaps 0;
 Matches 352; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MESSGRPSLCOFILGTTSVVTAALYSVYRQKARVSQELKGAKKVHLEBDLKSILSEAPG 60
 DB 1 MESSGRPSLCOFILGTTSVVTAALYSVYRQKARVSQELKGAKKVHLEBDLKSILSEAPG 60
 QY 61 KCVPAVIEGAVRSVKETLNSQFVENCQVIGRLTQEHKVMWNRTHLMNDCSKIHOR 120
 DB 61 KCVPAVIEGAVRSVKETLNSQFVENCQVIGRLTQEHKVMWNRTHLMNDCSKIHOR 120
 QY 121 TMTVPFDLVPHEDGVDAVAVRLKPLDSVDLGLEYEKEFHSIQSFDTVIGHYISGERPK 180
 DB 121 TMTVPFDLVPHEDGVDAVAVRLKPLDSVDLGLEYEKEFHSIQSFDTVIGHYISGERPK 180
 QY 121 TMTVPFDLVPHEDGVDAVAVRLKPLDSVDLGLEYEKEFHSIQSFDTVIGHYISGERPK 180
 DB 121 TMTVPFDLVPHEDGVDAVAVRLKPLDSVDLGLEYEKEFHSIQSFDTVIGHYISGERPK 180
 QY 181 GIQETEMLKVGATLTGVELVLDNNSVRLQPPKQMYLSSQDPDSLQROESSVRLM 240
 DB 181 GIQETEMLKVGATLTGVELVLDNNSVRLQPPKQMYLSSQDPDSLQROESSVRLM 240
 QY 241 KVLALVFQATCATLFFILRKQYLOERLRLKQOEBOEHEAQLLSRAKPEDRESLKS 300
 DB 241 KVLALVFQATCATLFFILRKQYLOERLRLKQOEBOEHEAQLLSRAKPEDRESLKS 300
 QY 301 ACVCLSSFKSCVFLFCGHVCSCTECYRALPEPKKPCICRAITRVIPLNYS 352
 DB 301 ACVCLSSFKSCVFLFCGHVCSCTECYRALPEPKKPCICRAITRVIPLNYS 352

RESULT 2
 Q7Z431 HUMAN
 ID Q7Z431 HUMAN PRELIMINARY; PRT; 352 AA.
 AC Q7Z431;
 DT 01-OCT-2003 (TrEMBLrel. 25, Created)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Putative NFkB activating protein.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
 OC Homo.
 NCBI_TaxID=9606;
 RX MEDLINE=22646590; PubMed=12761501; DOI=10.1038/sj.onc.1206406;
 RA Matsuda A., Suzuki Y., Honda G., Muramatsu S., Matsuzaki O.,
 RA Nagano Y., Doi T., Shimochino K., Harada T., Nishida E., Hayashi H.,
 RA Sugano S.;
 RT "Large-scale identification and characterization of human genes that
 activate NF-kappaB and MAPK signaling pathways.";
 RT Oncogene 22:3307-3318(2003).
 RL EMBL: AB097015; BAC7368.1; -; mRNA.

DR Ensembl; ENSG0000090432; Homo sapiens.
 DR GO: GO:000151; C: ubiquitin ligase complex; IEA.
 DR GO: GO:0046872; F: metal ion binding; IEA.
 DR GO: GO:0004842; F: ubiquitin-protein ligase activity; IEA.
 DR GO: GO:0008270; F: zinc ion binding; IEA.
 DR GO: GO:0016567; P: protein ubiquitination; IEA.
 DR InterPro: IPR001841; Znf_RING.
 DR SMART: SM00184; RING_1.
 DR PROSITE: PS50089; ZF_RING_2; 1.
 KM Metal-binding; Zinc; Zinc-finger.
 SQ SEQUENCE 352 AA; 39784 MW; 6EF2B8BCE1801F CRC64;

Query Match 99.6%; Score 1824; DB 2; Length 352;
 Best Local Similarity 99.7%; Pred. No. 1.1e-128;
 Matches 351; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MESSGRPSLCOFILGTTSVVTAALYSVYRQKARVSQELKGAKKVHLEBDLKSILSEAPG 60
 DB 1 MESSGRPSLCOFILGTTSVVTAALYSVYRQKARVSQELKGAKKVHLEBDLKSILSEAPG 60
 QY 61 KCVPAVIEGAVRSVKETLNSQFVENCQVIGRLTQEHKVMWNRTHLMNDCSKIHOR 120
 DB 61 KCVPAVIEGAVRSVKETLNSQFVENCQVIGRLTQEHKVMWNRTHLMNDCSKIHOR 120
 QY 121 TMTVPFDLVPHEDGVDAVAVRLKPLDSVDLGLEYEKEFHSIQSFDTVIGHYISGERPK 180
 DB 121 TMTVPFDLVPHEDGVDAVAVRLKPLDSVDLGLEYEKEFHSIQSFDTVIGHYISGERPK 180
 QY 181 GIQETEMLKVGATLTGVELVLDNNSVRLQPPKQMYLSSQDPDSLQROESSVRLM 240
 DB 181 GIQETEMLKVGATLTGVELVLDNNSVRLQPPKQMYLSSQDPDSLQROESSVRLM 240
 QY 241 KVLALVFQATCATLFFILRKQYLOERLRLKQOEBOEHEAQLLSRAKPEDRESLKS 300
 DB 241 KVLALVFQATCATLFFILRKQYLOERLRLKQOEBOEHEAQLLSRAKPEDRESLKS 300
 QY 301 ACVCLSSFKSCVFLFCGHVCSCTECYRALPEPKKPCICRAITRVIPLNYS 352
 DB 301 ACVCLSSFKSCVFLFCGHVCSCTECYRALPEPKKPCICRAITRVIPLNYS 352

RESULT 3
 Q9H9B5 HUMAN
 ID Q9H9B5 HUMAN PRELIMINARY; PRT; 352 AA.
 AC Q9H9B5;
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Hypothetical protein FLJ12875.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
 OC Homo.
 NCBI_TaxID=9606;
 RX PubMed=14702039; DOI=10.1038/ng1285;
 RA Ota T., Suzuki Y., Nishikawa T., Otsuki T., Sugiyama T., Irie R.,
 RA Makamatsu A., Hayashi K., Sato H., Nagai K., Kimura K., Makita H.,
 RA Sekine M., Ohtsuka M., Nishi T., Shibahara T., Tanaka T., Ishii S.,
 RA Yamamoto J., Ii, Saito K., Kawai Y., Isono Y., Nakamura Y.,
 RA Nagahari K., Murakami K., Yasuda T., Iwayanagi T., Wagatsuma M.,
 RA Shiratori A., Sudo H., Hosoiri T., Kaku Y., Kodaira H., Kondo H.,
 RA Sugawara M., Takahashi M., Kanda K., Yokoi T., Furuya T., Kikawa E.,
 RA Omura Y., Abe K., Kamihara K., Katsura N., Sato K., Tanikawa M.,
 RA Yamazaki M., Nishimura K., Ishibashi T., Yamashita H., Murakawa M.,
 RA Fujimori K., Tanai H., Kimata M., Watanabe M., Hirakawa S., Chiba Y.,
 RA Ishida S., Ono Y., Takiguchi S., Watanabe S., Yoisida M., Hottura T.,
 RA Kusano Y., Kanehori K., Takahashi-Fujii A., Hara H., Tanase T.-O.,
 RA Nomura Y., Togiyasu K., Komai F., Hara R., Takeuchi K., Arita M.,
 RA Imose N., Mueshino K., Yuki H., Ohnima A., Saeki N., Aotsuka S.,
 RA Yoshioka Y., Matsunawa H., Ichihara T., Shiohara N., Sano S.,
 RA Moriya S., Momiyama H., Satoh N., Takami S., Terashima Y., Suzuki O.,

RA Nakagawa S., Senoh A., Mizoguchi H., Goto Y., Shimizu F., Wakebe H.,
 RA Hisigaki H., Watanabe T., Sugiyama A., Takemoto M., Kawakami B.,
 RA Yamazaki M., Watanabe K., Kumagai A., Itakura S., Fukuzumi Y.,
 RA Fujimori Y., Komiyama M., Tashiro H., Taniguchi A., Fujiwara T.,
 RA Ono T., Yamada K., Fujii Y., Ozaki K., Hirao M., Omori Y.,
 RA Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,
 RA Okitani R., Kawakami T., Noguchi S., Itoh T., Shigeta K., Senba T.,
 RA Matsumura K., Nakajima Y., Mizuno T., Morinaga M., Sasaki M.,
 RA Togsashi T., Oyama M., Hata H., Watanabe M., Komatsu T.,
 RA Mizushima-Sugano J., Satoh T., Shirai Y., Takahashi Y., Nakagawa K.,
 RA Okumura K., Nagase T., Nomura N., Kikuchi H., Masuno Y., Yamashita R.,
 RA Nakai K., Yada T., Nakamura Y., Ohara O., Isogai T., Sugano S.,
 RT "Complete sequencing and characterization of 21,243 full-length human
 RT cDNAs".
 RL Nat. Genet. 36:40-45(2004).
 DR EMBL: AK022937; BAB14317.1; -; mRNA.
 DR GO: GO:0000151; Cubitiquitin ligase complex; IEA.
 DR GO: GO:0046872; E-metal ion binding; IEA.
 DR GO: GO:0004842; E-ubiquitin-protein ligase activity; IEA.
 DR GO: GO:0008270; E-zinc ion binding; IEA.
 DR GO: GO:0015657; E-protein ubiquitination; IEA.
 DR InterPro: IPR001841; ZnF_RING.
 DR SMART: SM00184; RING; 1.
 DR PROSITE: PS50089; ZF_RING_2; 1.
 KM Metal-binding; Zinc; Zinc-finger.
 SQ SEQUENCE 352 AA; 39717 MW; C19P150D278C2DA9 CRC64;

Query Match 99.3%; Score 1818; DB 2; Length 352;
 Best Local Similarity 99.7%; Pred. No. 3.2e-128;
 Matches 351; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MESSGRPSLCQFILGTTSVTALYSYVRKARVSQELKAKVHLGSDLSISEAG 60
 DB 1 MESSGRPSLCQFILGTTSVTALYSYVRKARVSQELKAKVHLGSDLSISEAG 60
 QY 61 KCPYAVIEGAVRSYKETLNSQFVENCCKGVQRLTLOSHKWMNRTTHLMDCKSIHOR 120
 DB 61 KCPYAVIEGAVRSYKETLNSQFVENCCKGVQRLTLOSHKWMNRTTHLMDCKSIHOR 120
 QY 121 TWTVPFDLVPHEDGDVAVRVLPKLDSDVLGLETVYEKHPISQSFDTVIGHYISGERPK 180
 DB 121 TWTVPFDLVPHEDGDVAVRVLPKLDSDVLGLETVYEKHPISQSFDTVIGHYISGERPK 180
 QY 181 GIQETEMLKVGATLTGVELVDNNSVRLQPPKQMGYYLSSQFDSLQROESSVRLM 240
 DB 181 GIQETEMLKVGATLTGVELVDNNSVRLQPPKQMGYYLSSQFDSLQROESSVRLM 240
 QY 241 KYLALVFGPATCATLFFILRKQYLOROERLRLKQOEEOEHOEAOULLSRAKPEDRESLKS 300
 DB 241 KYLALVFGPATCATLFFILRKQYLOROERLRLKQOEEOEHOEAOULLSRAKPEDRESLKS 300
 QY 301 ACVCLISFSPKSCVPLECGHVCSTECYRALPEPKKPCICROAITRIVIPLYNS 352
 DB 301 ACVCLISFSPKSCVPLECGHVCSTECYRALPEPKKPCICROAITRIVIPLYNS 352

RESULT 4
 Q4R7G8_MACEFA PRELIMINARY; PRT; 352 AA.
 AC Q4R7G8;
 DT 13-SEP-2005 (TREMBlrel. 31, Created)
 DT 13-SEP-2005 (TREMBlrel. 31, Last sequence update)
 DE 13-SEP-2005 (TREMBlrel. 31, Last annotation update)
 DE Testis cDNA, clone: Q5A-15365, similar to human hypothetical protein
 FLJ12875 (FLJ12875).
 OS Macaca fascicularis (Crab eating macaque) (Cynomolpus monkey).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 OC Cercopithecoidea; Cercopithecoidea; Macaca.
 OC NCB1_TaxID=9541;
 RP NUCLEOTIDE SEQUENCE.
 RP International consortium for macaque cDNA sequencing, analysis;

RT "DNA sequences of macaque genes expressed in brain or testis and its
 RT evolutionary implications";
 RT Submitted (JUN-2005) to the EMBL/Genbank/DBJ databases.
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RA Osada N., Hirata M., Tanuma R., Kusuda J., Hida M., Suzuki Y.,
 RA Sugano S., Gojobori T., Shen J.C.-K., Wu C.I., Hashimoto K.;
 RT "Substitution rate and structural divergence of 5'UTR evolution:
 RT Comparative analysis between human and cynomolgus monkey cDNAs".
 RL Submitted (MAR-2004) to the EMBL/Genbank/DBJ databases.
 DR EMBL: AB168850; BA000954.1; -; mRNA.
 DR InterPro: IPR001841; ZnF_RING.
 DR PROSITE: PS50089; ZF_RING_2; 1.
 KM Hypothetical protein; Metal-binding; Nuclear protein; Zinc;
 KM Zinc-finger.
 SQ SEQUENCE 352 AA; 39827 MW; 4AB6245101E3B0D2 CRC64;

Query Match 99.1%; Score 1815; DB 2; Length 352;
 Best Local Similarity 99.1%; Pred. No. 5.3e-128;
 Matches 349; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MESSGRPSLCQFILGTTSVTALYSYVRKARVSQELKAKVHLGSDLSISEAG 60
 DB 1 MESSGRPSLCQFILGTTSVTALYSYVRKARVSQELKAKVHLGSDLSISEAG 60
 QY 61 KCPYAVIEGAVRSYKETLNSQFVENCCKGVQRLTLOSHKWMNRTTHLMDCKSIHOR 120
 DB 61 KCPYAVIEGAVRSYKETLNSQFVENCCKGVQRLTLOSHKWMNRTTHLMDCKSIHOR 120
 QY 121 TWTVPFDLVPHEDGDVAVRVLPKLDSDVLGLETVYEKHPISQSFDTVIGHYISGERPK 180
 DB 121 TWTVPFDLVPHEDGDVAVRVLPKLDSDVLGLETVYEKHPISQSFDTVIGHYISGERPK 180
 QY 181 GIQETEMLKVGATLTGVELVDNNSVRLQPPKQMGYYLSSQFDSLQROESSVRLM 240
 DB 181 GIQETEMLKVGATLTGVELVDNNSVRLQPPKQMGYYLSSQFDSLQROESSVRLM 240
 QY 241 KYLALVFGPATCATLFFILRKQYLOROERLRLKQOEEOEHOEAOULLSRAKPEDRESLKS 300
 DB 241 KYLALVFGPATCATLFFILRKQYLOROERLRLKQOEEOEHOEAOULLSRAKPEDRESLKS 300
 QY 301 ACVCLISFSPKSCVPLECGHVCSTECYRALPEPKKPCICROAITRIVIPLYNS 352
 DB 301 ACVCLISFSPKSCVPLECGHVCSTECYRALPEPKKPCICROAITRIVIPLYNS 352

RESULT 5
 O8VCM5_MOUSE PRELIMINARY; PRT; 352 AA.
 AC O8VCM5;
 DT 01-MAR-2002 (TREMBlrel. 20, Created)
 DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
 DE 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
 DE RIKEN cDNA 0610009K11.
 GN Name=0610009K11rik;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Muridae; Murinae; Mus.
 OC NCB1_TaxID=10090;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RP STRAIN=FVB/N; TISSUE=Liver;
 RC MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shemen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Scheffer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares W.B., Bonaldo M.F., Casavant T.L., Schetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kerteman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grumwood J., Schmutz J., Myers R.M.,
 RA Buterfield Y.S.N., Krzywinski M.I., Skalska U., Smallus D.E.,
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=FVB/N; TISSUE=Liver;
 RA Strausberg R.;
 RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC019516; AAH19516.1; -. mRNA.
 DR HSSP; P38398; 1JM7.
 DR Ensembl; ENSMUSG0000041241; Mus musculus.
 DR MGI; MGI:1915600; 0610009K11R1K.
 DR GO; GO:0016021; C:Integral to membrane; TAS.
 DR InterPro; IPR001841; Znf_RING.
 DR SMART; SMO0184; RING_1.
 DR PROSITE; PS50089; ZF_RING_2; 1.
 KW Metal-binding; Zinc; Zinc-finger.
 SQ SEQUENCE 352 AA; 39821 MW; F3FE5D4771E0B140 CRC64;
 Query Match 91.4%; Score 1673; DB 2; Length 352;
 Best Local Similarity 90.1%; Pred. No. 2.5e-117;
 Matches 317; Conservative 18; Mismatches 17; Indels 0; Gaps 0;
 QY 1 MESGGRSLCOFILGTTSTVTAALVYVYRKARVSGELGKARKVHLGDLKSLSEAPG 60
 DB 1 MESSGRSLQGVILLGTTSSWTAVALVYSYRKQAVDELKGAKKHLEGLDKGILSEAPG 60
 QY 61 KCVYAVIEGAVRSVKETLNSOFENCKGVIOELTIOEHMWNRTTHLMDCKSTIHQR 120
 DB 61 KCVYAVIEGAVRSVKETLNSOFENCKGVIOELTIOEHMWNRTTHLMDCKSTIHQR 120
 QY 121 TNYVPELVPHEDGVDAVAVLRLDSDVGLSTVYEKFPSSIOSEFVYGHYISGERPK 180
 DB 121 TNYVPELVPHEDGVDAVAVLRLDSDVGLSTVYEKFPSSIOSEFVYGHYISGERPK 180
 QY 121 TNYVPELVPHEDGVDAVAVLRLDSDVGLSTVYEKFPSSIOSEFVYGHYISGERPK 180
 DB 121 TNYVPELVPHEDGVDAVAVLRLDSDVGLSTVYEKFPSSIOSEFVYGHYISGERPK 180
 QY 181 GIOETEMLVKAGTALVSGELVLDNNSVRLQPRKQKQYLLSSQDPSLHROESSVRLM 240
 DB 181 GIOETEMLVKAGTALVSGELVLDNNSVRLQPRKQKQYLLSSQDPSLHROESSVRLM 240
 QY 241 KVLALVGFATCATLFFILRKQYLOERLRLKQOEEOEHRAOLLSSAKPEDRESLKS 300
 DB 241 KVLALVGFATCATLFFILRKQYLOERLRLKQOEEOEHRAOLLSSAKPEDRESLKS 300
 QY 241 KVLALVGFATCATLFFILRKQYLOERLRLKQOEEOEHRAOLLSSAKPEDRESLKS 300
 DB 241 KVLALVGFATCATLFFILRKQYLOERLRLKQOEEOEHRAOLLSSAKPEDRESLKS 300
 QY 301 ACVVCSSPFSKCYFLBEGHVCSTECYRALPEPKKCPICQATRVYIPLYNS 352
 DB 301 ACVVCSSPFSKCYFLBEGHVCSTECYRALPEPKKCPICQATRVYIPLYNS 352
 DB 301 ACVVCSSPFSKCYFLBEGHVCSTECYRALPEPKKCPICQATRVYIPLYNS 352

RESULT 6

Q8BHF2_MOUSE

Q8BHF2_MOUSE PRELIMINARY; PRT; 352 AA.

AC Q8BHF2; 01-MAR-2003 (Tremblrel. 23, Created)
 DT 01-MAR-2003 (Tremblrel. 23, Last sequence update)
 DT 01-FEB-2005 (Tremblrel. 29, Last annotation update)
 DE Mus musculus 10 days neonate cortex cDNA, RIKEN full-length enriched
 DE library, clone:A830089D08 product:hypothetical RING finger containing
 DE protein, full insert sequence (Mus musculus 0 day neonate head cDNA,
 DE RIKEN full-length enriched library, clone:4831423H02
 DE product:hypothetical RING finger containing protein, full insert
 DE sequence) (Mus musculus adult male liver tumor cDNA, RIKEN full-length
 DE enriched library, clone:C730031H18 product:hypothetical RING finger
 DE containing protein, full insert sequence).
 GN Name=0610009K11R1K;
 OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Muridae; Murinae; Mus.
 NC NCBI_TaxId=10090;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Cortex, Head, and Liver;
 RX MEDLINE=9279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
 RA Carninci P., Hayashizaki Y.;
 RT "High-efficiency full-length cDNA cloning.";
 RL Meth. Enzymol. 303:19-44 (1999).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Cortex, Head, and Liver;
 RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
 RA Kawai T., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Aizawa K., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Cavaletto T.,
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
 RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barni G.,
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 RA Gustincich S., Hill D.P., Hofmann M., Hume D.A., Kamita M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima Y., Mazzarelli U., Mombere P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schenbach C., Seya T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyokawa K., Wang K.H., Weitz C., Whitaker C., Wilting L.,
 RA Wyszynski-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohetsuki S.,
 RA Hayashizaki Y.;
 RT "Functional annotation of a full-length mouse cDNA collection.";
 RL Nature 403:685-690 (2001).
 RN [3]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Cortex, Head, and Liver;
 RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
 RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
 RA Nikaido I., Oatso N., Saito R., Suzuki H., Yamana K., Kiyosawa H.,
 RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schenbach C., Gojbori T.,
 RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
 RA Schiml L.M., Kanapin A., Matsuda H., Batalov S., Beisels K.W.,
 RA Blake J.A., Bradt D., Bruscia V., Chochia C., Corbani L.E., Cousins S.,
 RA Dalla E., Dragani T.A., Fletcher C.P., Forrest A., Frazer K.S.,
 RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
 RA Grummond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
 RA Kanai A., Kawai H., Kawasawa Y., Kedzierski R.M., King B.L.,
 RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
 RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
 RA Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
 RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramchandran S.,
 RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
 RA Sandelin A., Schneider C., Sempile C.A., Setou M., Shimada K.,
 RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
 RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
 RA Wilming L.G., Wyszynski-Boris A., Yanagisawa M., Yang I., Yang L.,
 RA Yuan Z., Zavalon M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
 RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
 RA Shiraki T., Waki K., Kawai T., Aizawa K., Arahata T., Fukuda S.,
 RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
 RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
 RA Yaunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
 RA Birney E., Hayashizaki Y.;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs.";
 RL Nature 420:563-573 (2002).
 RN [4]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Cortex, Head, and Liver;
 RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
 RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,

RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
 RT "Normalization and subtraction of cap-trapper-selected cDNAs to
 RT prepare full-length cDNA libraries for rapid discovery of new genes.";
 RL Genome Res. 10:1617-1630(2000).
 [5]
 RN NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=cortex, Head, and Liver;
 RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
 RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Saeki N., Carninci P.,
 RA Konno H., Akiyama J., Nishi K., Katsunari T., Tashiro H., Itoh M.,
 RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishino T., Harada A.,
 RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
 RA Fujiwara S., Inoue K., Togawa Y., Izawa E., Ohara E., Watanabe M.,
 RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuzawa S., Kawai J.,
 RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
 RT "RIKEN integrated sequence analysis (RISA) system-384-format
 RT sequencing pipeline with 384 multicapillary sequencer.";
 RL Genome Res. 10:1757-1771(2000).
 [6]
 RN NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Cortex;
 RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
 RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
 RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
 RA Horii F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
 RA Kato H., Kawai J., Kojima Y., Kondo S., Konno H., Konda M., Koya S.,
 RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
 RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
 RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
 RA Sasaki D., Shibata K., Shingawa A., Shiraki T., Sogabe Y., Tagami M.,
 RA Tagawa A., Toyota T., Yasunishi A., Muramatsu M., Hayashizaki Y.,
 RA Tomaru A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
 RA Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 RN NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Head, and Liver;
 RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
 RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
 RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
 RA Horii F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
 RA Kato H., Kawai J., Kojima Y., Kondo S., Konno H., Konda M., Koya S.,
 RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
 RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
 RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
 RA Sasaki D., Shibata K., Shingawa A., Shiraki T., Sogabe Y., Tagami M.,
 RA Tagawa A., Toyota T., Yasunishi A., Muramatsu M., Hayashizaki Y.,
 RA Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
 RN NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Brain;
 RA EMBL, AK076419; BAC36332.1; -; mRNA.
 RA EMBL, AK083295; BAC38848.1; -; mRNA.
 RA HSP, P38398; JMW.
 DR Ensembl; ENSMUSG000004241; Mus musculus.
 DR MGI; MGI:1915600; 0610009K1Rik.
 DR GO; GO:0016021; C.integral to membrane; TAS.
 DR InterPro; IPR001841; znf_RING.
 DR SMART; SM00184; RING_1.
 DR PROSITE; PS50089; ZF_RING_2; 1.
 DR Hypothetical protein; Metal-binding; Zinc; zinc-finger.
 SQ SEQUENCE 352 AA; 39835 MW; 252530F1BD917871 CRC64;

Query Match 91.3%; Score 1672; DB 2; Length 352;
 Best Local Similarity 89.8%; Pred. No. 3e-117;
 Matches 316; Conservative 19; Mismatches 17; Indels 0; Gaps 0;

QY 1 MESGSPSLCOFLLGTSVTAATSYVYRQKARVSOEKGAKVHLGDLKSLISEARG 60
 DB 1 MESGSPSLCOFLLGTSVTAATSYVYRQKARVSOEKGAKVHLGDLKSLISEARG 60
 QY 61 KCVPAVAVIGAVSVKFTINSQFVENCQGVIOQLTQEHKMWNRTHLMDCKSIHQR 120
 DB 61 KCVPAVAVIGAVSVKFTINSQFVENCQGVIOQLTQEHKMWNRTHLMDCKSIHQR 120
 QY 61 KCVPAVAVIGAVSVKFTINSQFVENCQGVIOQLTQEHKMWNRTHLMDCKSIHQR 120
 DB 61 KCVPAVAVIGAVSVKFTINSQFVENCQGVIOQLTQEHKMWNRTHLMDCKSIHQR 120

QY 121 TMTVPFDLVPHEDGVAVRVLKPLDSDYDLGLETFYEFKFPSPISQFTDIGHYISGERPK 180
 DB 121 TMTVPFDLVPHEDGVAVRVLKPLDSDYDLGLETFYEFKFPSPISQFTDIGHYISGERPK 180
 QY 181 GIQTEEMLVKQATLTGVGELVLDNNSVRLQPPKQGMQYIYSSQDFSLQROESSVRLW 240
 DB 181 GIQTEEMLVKQATLTGVGELVLDNNSVRLQPPKQGMQYIYSSQDFSLQROESSVRLW 240
 QY 241 KYLALVPEFATCATLFFILRRQYLOROERLKLKQOESEFOHEHQLSRAPDEDESLKS 300
 DB 241 KILVAVFPAFCATLFFILRRQYLOROERLKLKQOESEFOHEHQLSRAPDEDESLKS 300
 QY 301 ACVCLSNFKSCVFLKCHVCSGRCQYALAEPRKPCICREITRVIPLYNS 352
 DB 301 ACVCLSNFKSCVFLKCHVCSGRCQYALAEPRKPCICREITRVIPLYNS 352

RESULT 7
 Q9DCV9 MOUSE
 ID Q9DCV9 MOUSE PRELIMINARY; PRT; 352 AA.
 AC Q9DCV9
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)
 DT 01-JUN-2001 (TrEMBLrel. 24, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Mus musculus adult male kidney cDNA, RIKEN full-length enriched
 DE library, clone:0610009K11 product:hypothetical RING finger containing
 DE protein, full insert sequence.
 GN Name=0610009K11Rik;
 OS Mus musculus (Mouse)
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridea; Muridae; Murinae; Mus.
 OX NCBI_TaxId=10090;
 RN [1]
 RN NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Kidney;
 RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
 RA Carninci P., Hayashizaki Y.;
 RT "High-efficiency full-length cDNA cloning.";
 RL Meth. Enzymol. 303:19-44(1999).
 RN [2]
 RN NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Kidney;
 RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
 RA Kawai J., Shingawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Aizawa K., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaoka I.,
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
 RA Kadota K., Matsuda H.A., Ashburner M., Batálov S., Casavant T.,
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiya H.,
 RA Kuehl P., Lewis S., Maceno Y., Nikaide I., Pesole G., Quackenbush J.,
 RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
 RA Brownstein M.J., Bull C., Fletcher C., Fujita M., Gariboldi M.,
 RA Guernicich S., Hill D., Hofmann M., Hume D.A., Kamya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzaletti J., Momberts P.,
 RA Norone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,
 RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohetsuki S.,
 RA Hayashizaki Y.;
 RT "Functional annotation of a full-length mouse cDNA collection.";
 RL Nature 403:685-690(2001).
 RN [3]
 RN NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Kidney;
 RA The FANTOM Consortium.
 RA the RIKEN Genome Exploration Research Group Phase I & II Team;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs.";
 RL Nature 420:563-573(2002).
 RN [4]

RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Kidney;
 RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
 RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
 RA Kono H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
 RT "Normalization and subtraction of cap-trapper-selected cDNAs to
 RT prepare full-length cDNA libraries for rapid discovery of new genes.";
 RL Genome Res. 10:1617-1630(2000).
 RN [5].
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Kidney;
 RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
 RA Shibata K., Itoh M., Aizawa K., Nagao S., Sasaki N., Carninci P.,
 RA Kono H., Akiyama J., Nishi K., Kitamura T., Tashiro H., Itoh M.,
 RA Suni N., Ishii Y., Nakamura S., Hazama M., Nishino T., Harada A.,
 RA Yamamoto R., Matsunoto H., Sakaguchi S., Ilegami T., Kashiwagi K.,
 RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watabiki M.,
 RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,
 RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
 RT "RIKEN integrated sequence analysis (RISA) system-384-format
 RT sequencing pipeline with 384 multicapillary sequencer.";
 RL Genome Res. 10:1757-1771(2000).
 RN [6].
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Kidney;
 RA Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,
 RA Akakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
 RA Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hirooka T., Hoti F.,
 RA Inotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,
 RA Kawai J., Kojima Y., Kono H., Kouda M., Koya S., Kurihara C.,
 RA Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,
 RA Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai C., Sakai K.,
 RA Sano H., Sasaki D., Shibata K., Shibata Y., Shingawa K., Shiraki T.,
 RA Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,
 RA Tejima Y., Toya T., Yamamura T., Yamunishi A., Yoshida K., Yoshino M.,
 RA Muramatsu M., Hayashizaki Y.;
 RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AK002416; BAB22084.1; -; mRNA.
 DR HSSP: P38398; 1JW7.
 DR Ensembl: ENSMUSG00000041241; Mus musculus.
 DR MGI: MGI:1915500; 0610009K1R1K.
 DR GO: GO:0016021; C:integral to membrane; TMS.
 DR InterPro: IPR001841; Znf_RING.
 DR SMART: SM00184; RING; 1.
 DR PROSITE: PS50089; ZF_RING_2; 1.
 DR Hypothetical protein; Metal-binding; Zinc-finger.
 SQ SEQUENCE 352 AA; 39883 MW; 29933D46BD9165C6 CRC64;
 Query Match 91.0%; Score 1667; DB 2; Length 352;
 Best Local Similarity 89.5%; Pred. No. 7, 1e-117;
 Matches 315; Conservative 19; Mismatches 18; Indels 0; Gaps 0;
 QY 1 MESGSRPSLCOFILLGTTSTVTAALSYVRKARVSOELKGAKVILGSDLSIISEAG 60
 DB 1 MESGSRPSLCOVILLGTTSSMTVAVALSIRKQAVQELGAKKILGDLGIISEAG 60
 QY 61 KCYPYAVIEGAVSVKELTNSQFVENCQVIGLRLQEHKMNWNRTHLMNDSKIIHOR 120
 DB 61 KCYPYAVIEGAVSVKELTNSQFVENCQVIGLRLQEHKMNWNRTHLMNYSKIIHOR 120
 QY 121 TNNVPEDVPHNCGVAVRVLKPLDSVGLGTTVEKHPHSIQSTTVDIYGHISGERPK 180
 DB 121 TNNVPEDVPHNCGVAVRVLKPLDSVGLGTTVEKHPHSIQSTTVDIYGHISGERPK 180
 QY 122 TNNVPEDVPHNCGVAVRVLKPLDSVGLGTTVEKHPHSIQSTTVDIYGHISGERPK 180
 DB 122 TNNVPEDVPHNCGVAVRVLKPLDSVGLGTTVEKHPHSIQSTTVDIYGHISGERPK 180
 QY 181 GJOETEEMTKVAGTILGVGELVLDNNSVRLPPOPKQMGYYLSSODPDSLORQESSVRLM 240
 DB 181 GJOETEEMTKVAGTILGVGELVLDNNSVRLPPOPKQMGYYLSSODPDSLORQESSVRLM 240
 QY 241 KVLALVFGATCATLFFILRKQYLRQERLRLKQMEFQOEHAQQLSRAKPEDESLKS 300
 DB 241 KVLALVFGATCATLFFILRKQYLRQERLRLKQMEFQOEHAQQLSRAKPEDESLKS 300
 QY 301 ACVVCLSRKSQVFLGCHGVCSTECYRALPBRKCPICRQALITRVIPLYNS 352

DB 301 ACVVCLSRKSQVFLGCHGVCSTECYRALPBRKCPICRQALITRVIPLYNS 352
 RESULT 8
 Q6NTT6_XENIA PRELIMINARY; PRT; 353 AA.
 AC Q6NTT6;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE MG828282 protein.
 GN Name=MG8282;
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
 OC Xenopodinae; Xenopus; Xenopus.
 NC NCB1_Taxid=8355;
 RN [1].
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Kidney;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altshul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldi M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ueidi T.B., Toshyluk S., Carninci P., Prange C.,
 RA Raha S.S., Loguettano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
 RA Bosak S.A., McKernan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Bosak S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Kuzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy U., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzyzanski M.I., Skalska U., Smallus D.E.,
 RA Scherch A., Schein J.E., Jones S.J.W., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2].
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Kidney;
 RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
 RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
 RA Richardson P.;
 RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
 RT initiative.";
 RT Dev. Dyn. 225:384-391(2002).
 RN [3].
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Kidney;
 RA Klein S., Strausberg R.;
 RL Submitted (Apr-2004) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: Contains 1 RING-type zinc finger.
 DR EMBL: BC068869; AA68869.1; -; mRNA.
 DR GO: GO:0000151; C:ubiquitin ligase complex; IEA.
 DR GO: GO:0046872; F:metal ion binding; IEA.
 DR GO: GO:0004842; F:ubiquitin-protein ligase activity; IEA.
 DR GO: GO:0008270; F:zinc ion binding; IEA.
 DR GO: GO:0016567; P:protein ubiquitination; IEA.
 DR InterPro: IPR001841; Znf_RING.
 DR Pfam: PF00097; ZF-C3HC4; 1.
 DR SMART: SM00184; RING; 1.
 DR PROSITE: PS50089; ZF_RING_2; 1.
 DR Metal-binding; Ub1 conjugation pathway; Zinc-finger.
 SQ SEQUENCE 353 AA; 40359 MW; 102A3C761CDD7EFA CRC64;
 Query Match 69.8%; Score 1277.5; DB 2; Length 353;
 Best Local Similarity 64.9%; Pred. No. 1, 3e-87;
 Matches 229; Conservative 63; Mismatches 60; Indels 1; Gaps 1;

QY 1 MESSGRPSLCOPIILGTTSTVTAALYSYVYRORAKARYSOELKGAKVHLGEDLSILSEARG 60
 DB 1 MESSGRPSVGVVILTTSSAITLALFSTYRHKRYSVQTLKEAKFCLTDLPVAVSDLP 60
 QY 61 KCVPAVAVGAVRSVYKELTNSQFVENCXGVIORLTLOEHKVMWNRTHLMDNSKIIHOR 120
 DB 61 KCVPAVAVGAVRSVYKELTNSQFVENCXGVIORLTLOEHKVMWNRTHLMDNSKIIHOR 120
 QY 121 TMTVPDLVPHEDVDVAVRVLKPLDSDVLDGLETYKEKPHSIOGFTDVIYHIGSEGP 179
 DB 121 TMTVPDLVPHEDVDVAVRVLKPLDSDVLDGLETYKEKPHSIOGFTDVIYHIGSEGP 179
 QY 180 KGIOEEMKXGATLTGVELVDNNSVRLQPPKQOMGYLSSQOPDLSLROESSVRL 239
 DB 181 KGIOEEMKXGATLTGVELVDNNSVRLQPPKQOMGYLSSQOPDLSLROESSVRL 239
 QY 240 KVALVFPFATCATLFTILRKQYLOQRRLKQWEEFOEHEAQLSRAPEDRESLKS 299
 DB 241 KVALVFPFATCATLFTILRKQYLOQRRLKQWEEFOEHEAQLSRAPEDRESLKS 299
 QY 300 SACVCLSFKSCVFLFEGCHVCSCTECYRALPEPKKCPICRAITRVIPLVNS 352
 DB 301 NCSICLSRSCVFLFEGCHVCSCTECYRALPEPKKCPICRAITRVIPLVNS 352
 RESULT 9
 QAS6B4_TETNG PRT; 352 AA.
 ID QAS6B4_TETNG PRELIMINARY;
 AC QAS6B4;
 DT 13-SEP-2005 (TREMBlrel. 31, Created)
 DT 13-SEP-2005 (TREMBlrel. 31, Last sequence update)
 DT 13-SEP-2005 (TREMBlrel. 31, Last annotation update)
 DE Chromosome 9 SCAR14729, whole genome shotgun sequence.
 DE (Fragment).
 GN ORFNames=GSTENG00023363001;
 OS Tetradodon nigrovittatus (Green puffer).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetradontiformes;
 OC Tetradontidae; Tetradontidae; Tetradontidae;
 OC NCB1_Taxid=99883;
 RN [1]
 RA NUCLEOTIDE SEQUENCE.
 RA Jallou O., Aury J.M., Brunet F., Petit J.L., Strange-Thomann N.,
 RA Mauceli E., Bouneau L., Fischer C., Oufou-Costaz C., Bernot A.,
 RA Nicard S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,
 RA Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,
 RA Anthouard V., Jubin C., Castellani V., Katinka M., Vacherie B.,
 RA Biemont C., Skell Z., Cattolico L., Poulin J., De Bernardis V.,
 RA Crund C., Duprat S., Broctier P., Coutanceau J.P., Gouzy J.,
 RA Parra G., Lardier G., Chappie C., McKernan K.J., McEwan P., Bosak S.,
 RA Kellis M., Volff J.N., Guigo R., Zody M.C., Mesirov J.,
 RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
 RA Lander V., Schacher V., Quetier F., Saurin W., Scarpelli C.,
 RA Wincker P., Lander E.S., Weissbach J., Roest Croliun H.,
 RA "Genome duplication in the teleost fish Tetradodon nigrovittatus reveals
 RA the early vertebrate proto-tetraploidy".
 RA Nature 431:946-957(2004).
 RN [2]
 RA NUCLEOTIDE SEQUENCE.
 RA Genoscope, Whitehead Institute Centre for Genome Research;
 RA Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
 CC -1- CAUTION: The sequence shown here is derived from an
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
 DR EMBL; CAAB01014729; CAG03818.1; -; Genomic_DNA.
 FT NON TER 352 352 82P8A5E08C53F4 CRC64;
 SQ SEQUENCE 352 AA; 3986 MM; 82P8A5E08C53F4 CRC64;
 Query Match 62.5%; Score 1145; DB 2; Length 352;
 Best Local Similarity 59.4%; Pred. No. 1.2e-77;
 Matches 209; Conservative 55; Mismatches 88; Indels 0; Gaps 0;

QY 1 MESSGRPSLCOPIILGTTSTVTAALYSYVYRORAKARYSOELKGAKVHLGEDLSILSEARG 60
 DB 1 MESSGRPSVGVVILTTSSAITLALFSTYRHKRYSVQTLKEAKFCLTDLPVAVSDLP 60
 QY 61 KCVPAVAVGAVRSVYKELTNSQFVENCXGVIORLTLOEHKVMWNRTHLMDNSKIIHOR 120
 DB 61 KCVPAVAVGAVRSVYKELTNSQFVENCXGVIORLTLOEHKVMWNRTHLMDNSKIIHOR 120
 QY 121 TMTVPDLVPHEDVDVAVRVLKPLDSDVLDGLETYKEKPHSIOGFTDVIYHIGSEGP 180
 DB 121 TMTVPDLVPHEDVDVAVRVLKPLDSDVLDGLETYKEKPHSIOGFTDVIYHIGSEGP 180
 QY 181 KGIOEEMKXGATLTGVELVDNNSVRLQPPKQOMGYLSSQOPDLSLROESSVRL 240
 DB 181 KGIOEEMKXGATLTGVELVDNNSVRLQPPKQOMGYLSSQOPDLSLROESSVRL 240
 QY 241 KVALVFPFATCATLFTILRKQYLOQRRLKQWEEFOEHEAQLSRAPEDRESLKS 300
 DB 241 KVALVFPFATCATLFTILRKQYLOQRRLKQWEEFOEHEAQLSRAPEDRESLKS 300
 QY 301 ACVCLSFKSCVFLFEGCHVCSCTECYRALPEPKKCPICRAITRVIPLVNS 352
 DB 301 VCSICLSRSCVFLFEGCHVCSCTECYRALPEPKKCPICRAITRVIPLVNS 352
 RESULT 10
 QSM7X9_BRARE PRT; 341 AA.
 ID QSM7X9_BRARE PRELIMINARY;
 AC QSM7X9;
 DT 01-FEB-2005 (TREMBlrel. 29, Created)
 DT 01-FEB-2005 (TREMBlrel. 29, Last sequence update)
 DT 01-FEB-2005 (TREMBlrel. 29, Last annotation update)
 DE Hypothetical protein zgc:92166.
 DE ORFNames=zgc:92166;
 GN Brachydanio rerio (Zebrafish) (Danio rerio).
 OS Brachydanio rerio (Zebrafish) (Danio rerio).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
 OC Cyprinidae; Danio.
 OC NCB1_Taxid=7955;
 RN [1]
 RA NUCLEOTIDE SEQUENCE.
 RA Tissue=Whole;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Schein C.M., Schuler G.D.,
 RA Altshul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Mustina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.B.,
 RA Brownstein M.J., Uebli T.B., Toshitoki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Huiyk S.W.,
 RA Villalón D.K., Muzny K.C., Hale S., Sodergren B.J., Lu X., Gibbs R.A.,
 RA Fanny J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butlerfield V.S.N., Krzywinski M.I., Skalska J., Smallos D.E.,
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.,
 RA "Generation and initial analysis of more than 15,000 full-length human
 RA and mouse cDNA sequences".
 RA Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RA NUCLEOTIDE SEQUENCE.
 RA Tissue=Whole;
 RC NIH MGC Project;
 RC Submitted (DEC-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC088385; AA88385.1; -; mRNA.
 DR EMBL; ENSDARG0000021398; Danio rerio.
 DR ZFIN; ZDB-GENE-050102-5; zgc:92166.
 DR GO; GO:0000151; Cytubulin ligase complex; IEA.

DR GO:0046872; F-metal ion binding; IEA.
 DR GO:0004842; F-ubiquitin-protein ligase activity; IEA.
 DR GO:0008270; Zinc ion binding; IEA.
 DR GO:0015557; P-protein ubiquitination; IEA.
 DR InterPro:IPR001841; ZnF_RING.
 DR PROSITE:PS50089; ZF_RING_2.
 KW Hypothetical protein; Metal-binding; Nuclear protein; Zinc;
 KW Zinc-finger.
 SQ SEQUENCE 341 AA; 38585 MW; 4807666981CFD70 CRC64;

Query Match 42.4%; Score 776; DB 2; Length 341;
 Blast Local Similarity 43.9%; Pred. No. 6.3e-50;
 Matches 151; Conservative 72; Mismatches 109; Indels 12; Gaps 5;

QY 11 QPILGTSVVAALAYSVYRQKARVSOELKGAKKVHIGEDKSLSEAPGCVAYVIEG 70
 DB 8 EAVCGSSVALSGLFYIRKKRVKDKAPVWALDAKLIDILMTPGCKLOLVVVEG 67
 QY 71 AVRSYKELTNSQFVENCQVITQRLTQEHKVMNRTHLMDCKSIHQRTNTPFDLVP 130
 DB 68 TVQPVGEPLRSQFQSSVGVIOKLVLRHKLVMNSLGRITWDSRVLLQRNAVFPML- 126
 QY 131 HEDGVDA-VVILKPLDSDVGLQETVYKHPISQSPFDVYGHYISGEPKGIQETEMT 189
 DB 127 ---GLNKFVAYLCLEATGPKMEIVHEKFKQATVYGTDLIGYLSGKPKGQLETEM 183
 QY 190 KVGAATLTVGSELVDNNS-VRLQPPKQMQYTLSSQFDSLQROESSVRLMKVLAIVFG 248
 DB 184 KVGASLTVVGGELIDTLRLKIRPPDQSEVFLLSSAPFTILMEQEQAEVWRFACICA 243
 QY 249 FATCATLFFILKQYLQROELRLKQOEQOEHEAQLLSRANKREDRSKSAQVCLSS 308
 DB 244 LAGVAVLWTRRRYRQKLKMEQENLRREFG----MGTGEHEEDNGVENACVICLSN 298
 QY 309 FKSCVFLGCHVSCCTEYRALPEPKKCPICROAITVPIVLYNS 352
 DB 299 PRGCVLLDCGHVCCPCFCYQALPQP-FCPICRHKKRVPLVLA 341

RESULT 11
 Q9VZJ9 DROME
 ID Q9VZJ9 DROME PRELIMINARY; PRT; 338 AA.
 AC Q9VZJ9

DT 01-MAY-2000 (TrEMBL:rel. 13, Created)
 DT 01-MAY-2000 (TrEMBL:rel. 13, Last sequence update)
 DT 10-MAY-2005 (TrEMBL:rel. 10, Last annotation update)
 DE CG1134-PA (AT15655D).
 GN ORFNames=CG1134, CG1134;
 OS Drosophila melanogaster (fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 (1)
 NP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=20196006; Pubmed=10731132; DOI=10.1126/science.287.5461.2185;
 RA Adams M.D., Celnikier S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blazer R.G., Champe M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., McKus G.L.G.,
 RA Abril J.F., Agbayani A., An H.-J., Andrews-Panichok C., Baldwin D.,
 RA Ballow R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Bereman B.P., Bhandari D., Bolshakov S.,
 RA Borkova D., Botchan M.R., Bouck H., Brokstein P., Brottier P.,
 RA Burris K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup I.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 RA Foster C., Gabrielian A.E., Gary N.S., Gelbart W.M., Glaser K.,
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,

RA Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kenison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Mishina N.V., Moadary C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Pacleb J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissenbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of Drosophila melanogaster.";
 RL Science 287:2185-2195 (2000).
 RN [2]

NP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=22426065; Pubmed=12537568;
 RA Celnikier S.E., Wheeler D.A., Krommiller B., Carlson J.W., Halpern A.,
 RA Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A.,
 RA George R.A., Hoskins R.A., Laverly T., Muzny D.M., Nelson C.R.,
 RA Pacleb J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,
 RA Svirskas R., Taber S., Wan K., Stapleton M., Sutton G.G., Venter C.,
 RA Weinstein G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.,
 RT "Finishing a whole-genome shotgun: release 3 of the Drosophila
 genome Biol. 3:RESEARCH0079-RESEARCH0079 (2002).
 RN [3]

NP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=22426070; Pubmed=12537573;
 RA Kaminker J.S., Bergman C.M., Krommiller B., Carlson J.W., Svirskas R.,
 RA Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,
 RA Ashburner M., Celnikier S.E.;
 RT "The transposable elements of the Drosophila melanogaster euchromatin:
 a genomes perspective.";
 RL Genome Biol. 3:RESEARCH0084.1-RESEARCH0084.20 (2002).
 RN [4]

NP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=22426069; Pubmed=12537572;
 RA Miya S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
 RA Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochuk S.E.,
 RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,
 RA Bettencourt B.R., Celnikier S.E., de Grey A.D.N.J., Drysdale R.A.,
 RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
 RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
 RA Lewis S.E.;
 RT "Annotation of the Drosophila melanogaster euchromatic genome: a
 systematic review.";
 RL Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22 (2002).
 RN [5]

NP NUCLEOTIDE SEQUENCE.
 RG Berkeley Drosophila Genome Project;
 RA Celnikier S., Carlson J., Wan K., Pfeiffer B., Frise E., George R.,
 RA Hoskins R., Stapleton M., Pacleb J., Park S., Svirskas R., Smith E.,
 RA Yu C., Rubin G.;
 RT "Drosophila melanogaster release 4 sequence.";
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 RN [6]

NP NUCLEOTIDE SEQUENCE.
 RG FlyBase;
 RL Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.
 RN [7]

NP NUCLEOTIDE SEQUENCE.
 RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
 RA Champe M., Chavez C., Dorsett V., Drensek D., Farfan D., Frise E.,
 RA George R., Gonzalez M., Guatin H., Krommiller B., Li P., Liao G.,
 RA Miranda A., Mungall C.J., Nunoo J., Pacleb J., Paragas V., Park S.,

Query Match	24.2%;	Score 442.5;	DB 2;	Length 338;
Best Local Similarity	30.6%;	Pred. No. 7.2e-25;		
Matches 104;	Conservative 74;	Mismatches 143;	Indels 19;	Gaps 8;

Q7Q6A1 ANOGA
ID Q7Q6A1_ANOGA PRELIMINARY; PRT; 339 AA.

DT 01-MAR-2004 (TREMBlrel. 26, Created)
DT 01-MAR-2004 (TREMBlrel. 26, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE ENSANGP00000010763.
GN ORENAMES=ENSANGP00000008274;
OS Anopheles gambiae str. PEST.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoides; Culicidae
OC Anophelinae; Anopheles.
OX NCBI_TaxID=180454;
RN [1]
RP NOCLEOTIDE SEQUENCE.
RP STRAIN=PEST;
RC The Anopheles gambiae Sequence Committee;
RG "Anopheles gambiae re-annotation."
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.

Query Match	23.8%	Score 436;	DB 2;	Length 339;
Best Local Similarity	31.5%	Pred. No. 2-2e-24;		
Matches 107	Conservation 149	Indels 18	Gaps 6	

RESULT 13
Q4RV85 TETNG
ID Q4RV85_TETNG PRELIMINARY;
PRT; 206 AA

DT 13-SEP-2005 (TREMBL:rel. 31, Created)
 DT 13-SEP-2005 (TREMBL:rel. 31, Last sequence update)
 DT 13-SEP-2005 (TREMBL:rel. 31, Last annotation update)
 DE Chromosome 15 SCAP14992, whole genome shotgun sequence.
 GN ORFNames=GSTENG00026438001;
 OS Tetraodon nigroviridis (Green puffer).
 OC Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
 OC Actinopterygii, Neopterygii, Teleostei, Euteleostei, Neoteleostei,
 OC Acanthomorphi, Acanthopterygii, Percomorpha, Tetraodontiformes,
 OC Tetraodonidae, Tetraodontidae, Tetraodon.
 CX NCBI_TaxID=99863;
 XM [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Jallion O., Aury J.M., Brunet F., Petit J.L., Strange-Thomann N.,
 RA Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Benoit A.,
 RA Nicard S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,
 RA Daillay C., Salanoubat M., Levy M., Boudet N., Castellano S.,
 RA Anthonard V., Jablin C., Castell J.V., Katinka M., Vacheffe B.,
 RA Biemont C., Skalli Z., Catolico L., Poulin J., De Bernardinis V.,
 RA Craud C., Duprat S., Broclet F., Coucaneau J.P., Gouy P.,
 RA Parra G., Lardier G., Chapple C., McKernan K.J., McSwan P., Bosak S.

RA Kellis M., Voif J.N., Guigo R., Zody M.C., Mesirov J.,
 RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
 RA Landet V., Schachter V., Queller F., Saurin W., Scarpelli C.,
 RA Winkler P., Lander E.S., Weissbach J., Roest Crollius H.,
 RT "Genome duplication in the teleost fish Tetraodon nigroviridis reveals
 RT the early vertebrate proto-karyotype." ;
 RL Nature 431:946-957(2004).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RG Genoscope: Whitehead Institute Centre for Genome Research;
 RL Submitted (Feb-2004) to the EMBL/GenBank/DBJ databases.
 CC -1- CAUTION: The sequence shown here is derived from an
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
 CC -1- SIMILARITY: Contains 1 RING-type zinc finger.
 DR EMBL: CA60104992; CAG07697.1; -; Genomic_DNA.
 DR InterPro: IPR001841; Znf_RING.
 DR Pfam: PF00097; ZF-C3HC4_1.
 DR PROSITE: PS50089; ZF_RING_2; 1.
 KW Metal-binding; Nuclear protein; Ub1 conjugation pathway; Zinc;
 KW Zinc-finger.
 SQ SEQUENCE 206 AA; 23238 MW; FC2F07246247B46E CRC64;

Query Match 23.6%; Score 431.5; DB 2; Length 206;
 Best Local Similarity 41.0%; Pred. No. 2.6e-24;
 Matches 84; Conservative 44; Mismatches 70; Indels 7; Gaps 3;
 QY 152 LETVEYKHPISIQFTDVIYGHISGRPKIOETHEMLKYGATLTGVEGLVLDNNSVRL 210
 DB 1 MEMIHEKHFQVSSGLVIVIGQYLSGERPKQLETETHEMLKYGALVIGAGELVLAADGTL 60
 QY 211 QPPKQMGQYIISODPSSLQROESSVRLKVALVGFATCATLFEILKQYLOQERL 270
 DB 61 QPPDGGSEYPLSLDVFSLQGLKSAVMCMVLAVSALGLTAVLVWVCRRYYCHKAKR 120
 QY 271 RLKMOSEFOHEHAKQLSPKRPD-----RESLSKSAVYVCLSPKSVFLKCHVSCST 325
 DB 121 QLEERKIFERMSERPRVSPASVNLVEEVENICVICTYETPRNCITMDCGHVCCYS 180
 QY 326 CYRALPEPKKCPICRAITREVPILY 350
 DB 181 CYQALVQ-RKCPICRQDISRVPLH 204

RESULT 14
 O6PBA9 BRARE
 ID O6PBA9 BRARE PRELIMINARY; PRT; 283 AA.
 AC O6PBA9;
 DT 05-JUL-2004 (TREMBlrel. 27, Created)
 DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
 DT 25-OCT-2004 (TREMBlrel. 27, Last annotation update)
 DE LOC402879 protein (Fragment).
 GN Name=LOC402879;
 OS Brachydanio rerio (Zebrafish) (Danio rerio).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
 OC Cyprinidae; Danio.
 OX NCBI_TaxID=7955;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Kidney;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Scheiner C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.R.,
 RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
 RA Bosak S.A., McMan P.J., McKernan K.U., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywicki M.I., Skalska U., Smalins D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences." ;
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Kidney;
 RA Strausberg R.;
 RL Submitted (Oct-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL: BC059797; AAHS9797.1; -; mRNA.
 FT NON TER 1
 SQ SEQUENCE 283 AA; 31798 MW; CD3C66BB7B68350C CRC64;

Query Match 21.4%; Score 391.5; DB 2; Length 283;
 Best Local Similarity 37.2%; Pred. No. 3.9e-21;
 Matches 92; Conservative 45; Mismatches 103; Indels 7; Gaps 5;
 QY 13 ILGTTSTVYTAALYGVROKARVSGELKGAKKVHGEDLSKLSAPKCVPIAVIEAV 72
 DB 25 ICAGSCFAPSGFLYGLYSDKRLKLEIPFPQDHHLLILNNSKRLHYAVAGELV 84
 QY 73 RSVKETLNSQYENCKGVYIQLTLQEHKVMNRTHLWNDSKLIH--QRTNVPFDLY- 129
 DB 85 QAVGPISISSQYVPRCHGVLOKITVHEHMKVNSLLKSW--VSKYNNQQTNTVPELTLYQ 142
 QY 130 PHEGVDVAVYLRKLDSDVDLGLFVYKRPSPISQSFVDVGHYISGRPGIOETEML 189
 DB 143 POSFSIDVCARVDSFLESGLPQQVHRVNAEGLMDVALGELISGKPTALEEREDL 202
 QY 190 KVGATLTGVEGLVLDNNSV-RLQPPKQMGQYIISODPSSLQROESSVRLKVALVGF 248
 DB 203 RVGVPLTAFGEVLVEQEKIMRIQPPKQGRSVLLPSVDYNSMQHNSVNMKGLTYLFG 262
 QY 249 FATCATL 255
 DB 263 L-TGSTL 268

RESULT 15
 O6AX71 XENLA
 ID O6AX71 XENLA PRELIMINARY; PRT; 221 AA.
 AC O6AX71;
 DT 25-OCT-2004 (TREMBlrel. 28, Created)
 DT 25-OCT-2004 (TREMBlrel. 28, Last sequence update)
 DT 25-OCT-2004 (TREMBlrel. 28, Last annotation update)
 DE MGC83539 protein.
 GN Name=MGC83539;
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;
 OC Xenopodinae; Xenopus; Xenopus.
 OX NCBI_TaxID=8355;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Oocytes;
 RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
 RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
 RA Richardson P.;
 RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
 RT initiative." ;
 RL Dev. Dyn. 225:384-391(2002).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Oocytes;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Scheiner C.F., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

[illegible]

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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 24, 2006, 08:25:44 ; Search time 41 Seconds
(without alignments)
826.056 Million cell updates/sec

Title: US-09-978-360A-437

Perfect score: 1831

Sequence: 1 MESSGRPLCQFLLIGTTSV.....PKKCPICQATRVIPLYNS 352

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database :

1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	230.5	12.6	237	2 TS2432	hypothetical prote
2	201	11.0	383	2 P96582	hypothetical prote
3	138.5	7.6	115	2 B96664	probable RING zinc
4	138.5	7.6	618	2 S68450	apoptosis inhibito
5	137.5	7.5	604	2 S68449	apoptosis inhibito
6	136.5	7.5	316	2 T32659	hypothetical prote
7	134.5	7.3	428	2 T48167	hypothetical prote
8	131.5	7.2	358	2 JCS964	apoptosis inhibito
9	130	7.1	943	2 S68824	unknown protein, cyto
10	124.5	6.8	200	2 A96664	unknown protein, cyto
11	123	6.7	275	2 A45679	inhibitor-of-apopt
12	121.5	6.6	124	2 T01251	hypothetical prote
13	118	6.4	286	2 D36828	orl13 protein - Au
14	118	6.4	292	2 T41772	IAP1 orl27 - Bomby
15	117.5	6.4	824	2 T16028	hypothetical prote
16	116.5	6.4	268	2 T10304	inhibitor of apopt
17	116.5	6.4	268	2 A53989	apoptosis-inhibiti
18	116.5	6.4	299	2 T45881	hypothetical prote
19	116	6.3	433	2 UC7678	RING finger protei
20	115.5	6.3	739	2 E86434	protein F17F8.27 l
21	115	6.3	497	2 S69545	apoptosis inhibito
22	112.5	6.1	288	2 D97113	probable GTPase (Y
23	112.5	6.1	522	2 T18504	hypothetical prote
24	112	6.1	275	2 T10310	apoptosis-inhibiti
25	112	6.1	496	2 S68452	apoptosis-inhibiti
26	111	6.1	401	2 G96824	hypothetical prote
27	110.5	6.0	337	2 T48341	hypothetical prote
28	110	6.0	754	2 S35503	finger protein neu
29	110	6.0	797	2 AH1674	primosomal replica

30	107.5	5.9	529	2 T19204	hypothetical prote
31	107.5	5.9	753	2 S35371	finger protein neu
32	106.5	5.8	304	2 T10212	hypothetical prote
33	106.5	5.8	1133	1 S41478	DNA repair protein
34	105.5	5.8	234	2 T30427	probable apoptosis
35	105.5	5.8	489	2 T26069	hypothetical prote
36	104.5	5.7	202	2 T04906	hypothetical prote
37	104.5	5.7	780	2 T31548	hypothetical prote
38	104.5	5.7	823	2 D86165	protein p15K9.3 li
39	103.5	5.7	936	2 E71405	probable ankyrin -
40	103	5.6	711	2 C84767	hypothetical prote
41	102.5	5.6	1403	2 T17372	plasma membrane-as
42	102	5.6	132	2 B85092	hypothetical prote
43	102	5.6	797	2 AH1302	primosomal replica
44	100.5	5.5	131	2 T41790	AcNMPV orf44 - Bom
45	99.5	5.4	131	2 D72855	AcOrf-44 protein -

ALIGNMENTS

RESULT 1

TS2432 hypothetical protein ZCF61 [imported] - Arabidopsis thaliana

C/Species: Arabidopsis thaliana (mouse-ear cress)

C/Date: 24-Oct-2000 #sequence_revision 24-Oct-2000 #text_change 09-Jul-2004

C/Accession: TS2432

R/Kato, A.; Suzuki, M.; Kuwahara, A.; Ooe, H.; Higano-Inaba, K.; Komeda, Y.

Gene 239, 309-316, 1999

A/Title: Isolation and analysis of cDNA within a 300 kb Arabidopsis thaliana genomic reg

A/Reference number: 225171

A/Accession: TS2432

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: mRNA

A/Residues: 1-237 <KAT>

A/Cross-references: UNIPROT:Q9SLU0; UNIPARC:UPI00000A3331; EMBL:AB028228; PDB:BA07953.

A/Experimental source: cultivar Columbia

C/Genetics:

A/Map position: 1

A/Note: ZCF61

Query Match 12.6%; Score 230.5; DB 2; Length 237;
Best Local Similarity 29.9%; Pred. No. 4.6e-10;
Matches 75; Conservative 46; Mismatches 89; Indels 41; Gaps 15;

QY	121	TNTVPFDIVPHEDGVDAVRVLPKIDSDVLGL-----ETVYEKHPISIQSFTDVIQHYIS	175
DB	5	TKREVPMVL---DDGTG---RVNVDSQGLGIALTVGSDFEKAEP-VSLVQALG-YLK	56
QY	176	GERPKGIQETEMKLVGATLVGVELVLDN-NSVRALQPPKQGMQYLLSSQDPDSLQROE	234
DB	57	GKILIGVHVERVVDIGIPLVGAVRGNGNVAIQKEQD-PRVYVYIPIPDQLISKIG	115
QY	235	SSVRLMKVIAL---VEGFATCA--TLFPILRK--OYLROER-LRLKMQEERFQHEAQL	286
DB	116	DISRRFKASMGTLVGLVILSKYIEYLKRIEPTLRRRQRFALKVVD-----AA	168
QY	287	ISRAKP-----EDRESIKACVVCSSFKSCVFLGCGHVCSCTECYRALPEPKKPIC	339
DB	179	ARRAKPVTGGTSRGGTR-PDLCCVCLDQKVTARVECGHMCCTPCLQLT---RTCPIC	224
QY	340	ROATRVIPLY 350	
DB	225	RERIQOVAKIXY 235	

RESULT 2

P96582 hypothetical protein F1511.25 [imported] - Arabidopsis thaliana

C/Species: Arabidopsis thaliana (mouse-ear cress)

C/Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004

C/Accession: P96582

R/Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,

Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
 Aisen, N.F.; Hughes, B.; Hultzer, L.
 Nature 408, 816-820, 2000
 A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
 C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziani,
 Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
 A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
 Ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
 A:Title: Sequence and analysis of chromosome 1 of the plant *Arabidopsis*.
 A:Reference number: A86141; MUID:21016719; PMID:11130712
 A:Accession: F96582
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-383 <STO>
 A:Cross-references: UNIPROT:Q9SVH3; UNIPARC:UPI00000A0245; GB:AEO05173; NID:g4587558; PI
 A:Genetics:
 A:Gene: F1511.25
 A:Map position: 1

Query Match 11.0%; Score 201; DB 2; Length 383;
 Best Local Similarity 21.5%; Pred. No. 1.4e-07;
 Matches 81; Conservative 71; Mismatches 171; Indels 54; Gaps 13;
 14 ILGTTVTALYV-YRQKARQELKAKCHLGEGLKSLSEADKCP-----64
 23 ILGLTAVSAGSALKYASTNAALKIKDAPEVSI-SDLRSLPASEDKSETDNRKSD 81
 65 --YVIEGAVSVKETINSQFENCKGVIQRLTQEHKMNRTTHLMNCSKIHNR--120
 82 QRIVVAGVK--FKISGDEGKANNVILSPETDRLITQRTQTVYSQMKPLPOSTGH 139
 121 -----TNTPEPLVPHEDGV--VAVRV--LKPLDSVDLGLETVEKE 159
 140 RFMLERSLRKHGAFTRTVPVIVGKQDSNSFVAVMNGSQPLP-----LTTYVNL 194
 160 HPSIQSFVDVIGHYISERPKIOETEMLKVGATLTGVELVDNNSVFLQPPKQMQY 219
 195 QPINSFLQA--FLYPDYVGLIDIEKILPBGDITAVG-IYSPFNNGVEIKSCODLDP 250
 220 YLSSQDPSLQROESSVRLMKVLAIVGFATCATLFFILRKQYLRQERLRKQOEER 279
 251 FLSEMTDKMIEDMEQTNFPLIGSVILGIVSGILSYAVNRW---NKKMKMHOREI 306
 280 QEHNAQLISRAKPEDRESLSKA--CVCLSSFKSCVFLGCHVCSCTECYRALPEP--KK 335
 307 PQRPNDVSDPEPDADIEPDGELCVTSRRRVPAFIPGHVYVCCRCASTVERELNPK 366
 336 CPICRQATRVIPLYNS 352
 367 CPVCLQSIKSGMKVYIS 383

RESULT 3

B96664
 Probable RING zinc finger protein T12P18.8 [imported] - *Arabidopsis thaliana*
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C>Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
 C:Accession: B96664
 R:Theologos, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
 Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
 Aisen, N.F.; Hughes, B.; Hultzer, L.
 Nature 408, 816-820, 2000
 A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
 C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziani,
 Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
 A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
 Ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
 A:Title: Sequence and analysis of chromosome 1 of the plant *Arabidopsis*.
 A:Reference number: A86141; MUID:21016719; PMID:11130712
 A:Accession: B96664
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-115 <STO>

A:Cross-references: UNIPROT:Q9CAK3; UNIPARC:UPI00000A29C7; GB:AEO05173; NID:g6358794; P
 C:Species: Homo sapiens (man)
 A:Gene: T12P18.8
 A:Map position: 1

Query Match 7.6%; Score 138.5; DB 2; Length 115;
 Best Local Similarity 30.2%; Pred. No. 0.0015;
 Matches 35; Conservative 18; Mismatches 46; Indels 17; Gaps 4;
 248 GFATCATLFFILR--KOYLQERLRKQOEERQEHNAQLISRAKPEDRESLSKA---301
 2 GF-TVLGVFLITKHVIDSVLERRRRQQLKVLDAAKRAELSSGNSGNTSRISIDSTXK 60
 302 -----CVCLSSFKSCVFLGCHVCSCTECYRALPEPKCPICRQATRVIPLY 350
 61 EDAPVDLCVILCEQENAVFVPCGMCCCTACSSH---TSCPLCRRIIDLAVKTY 113

RESULT 4

S68450
 Apoptosis inhibitor hiap-2 - human
 C:Species: Homo sapiens (man)
 C>Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 09-Jul-2004
 C:Accession: S68450
 R:Liston, P.; Roy, N.; Tamai, K.; Lefebvre, C.; Baird, S.; Cherton-Horvat, G.; Farahani,
 Nature 379, 349-353, 1996
 A:Title: Suppression of apoptosis in mammalian cells by NAIP and a related family of IAP
 A:Reference number: A58182; MUID:96149249; PMID:8552191
 A:Accession: S68450
 A:Status: nucleic acid sequence not shown
 A:Molecule type: mRNA
 A:Residues: 1-618 <LIS>
 A:Cross-references: UNIPROT:Q13490; UNIPARC:UPI00000A435C; EMBL:U45879; NID:g1184317; PI
 A:Function: apoptosis suppressor
 A:Keywords: apoptosis; zinc finger
 C:Keywords: apoptosis; zinc finger
 F:567-611/Domain: RING zinc finger homology <RMG>

Query Match 7.6%; Score 138.5; DB 2; Length 618;
 Best Local Similarity 21.5%; Pred. No. 0.014;
 Matches 67; Conservative 50; Mismatches 119; Indels 75; Gaps 13;

82 QFVENCQVIOQLTQEHKMNRTTHLMNCSKIHORTNTPFDLVPHEHGDVAVRV 141
 343 EFVDEIQGRYHLL--EQLLSTDTTGENADPPIH-----FGGSSSDAVMM 391
 142 LKPL--DSVDLGL-----ETVEKEFHPISQSF--TDVIGHYISGERPKIQE---TE 186
 392 NTPVVKSLALEMGFNRLVKQTVLSKILTTGENYKTVNDIVSALINAEDEKEKEKQAE 451
 187 EMLKVGATLTGVGL-----VLDN-----NSVRLOPP--KQMQVYLSQD-FD 227
 452 EMASDLSLIRKNRAALFQQLTCVLPILIDNLKANVINKQHDIIKQTPILQAREID 511
 228 SLQROESSVRLMKVLAIVGFATCATLFFILRKQYLRQERL-----RLRKQOEERFQ 281
 512 TIWVGNAANVIFKCKLEIDSTLYKLFVDKMKKXIPTEBVSGLSLEQARRQOE---568
 282 HEAQLISRAKPEDRESLSKACVCLSSFKSCVFLGCHVCSCTECYRALPEPKCPICRQ 341
 569 -----RTCKVCMDEKVSVFIPCGHLVVCQBC--APSLRKCPICRG 607
 342 AITRVIPLYNS 352
 608 IIKGVKRTFLS 618

RESULT 5

S68449
 Apoptosis inhibitor hiap-1 - human
 C:Species: Homo sapiens (man)
 C>Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 09-Jul-2004
 C:Accession: S68449

R.Iliston, P.; Roy, N.; Tamai, K.; Lefebvre, C.; Baird, S.; Cherton-Horvat, G.; Farahani, Nature 379, 349-353, 1996
 A>Title: Suppression of apoptosis in mammalian cells by NAIp and a related family of IAP
 A:Reference number: A58182; MUID:96149249; PMID:8552191
 A:Accession: S68449
 A:Status: nucleic acid sequence not shown
 A:Molecule type: mRNA
 A:Residues: 1-604 <LIS>
 A:Cross-references: UNIPROT:Q13489; UNIPARC:UPI000004A35B; EMBL:U45878; MIM:G1184315; P
 C:Function:
 A:Description: apoptotic suppressor
 C:Keywords: apoptosis; zinc finger
 F:553-597/Domain: RING finger homology <RNG>

Query Match 7.5%; Score 137.5; DB 2; Length 604;
 Best Local Similarity 19.8%; Pred. No. 0.016;
 Matches 56; Conservative 52; Mismatches 94; Indels 81; Gaps 11;

QY 114 SKIHORTVTPEDLVPHEDGVDAVRVLPKPL--DSVDLGL-----ETVYEFKPSIOS 165
 DB 359 SSIH-----LEPGEDHSEDALIMATPVINAAMGFSRLVKQTVORKILATGEN 409
 QY 166 F--TDVIGHYISG-----ERPKGIQTEEMLVKGAATLVGVGLVLDNNSVRLQPKQ 215
 DB 410 YRLVNDLVLDLNAEDEIRBEERERATEKE-----SNDLLIRKNM 452
 QY 216 GMQYIL-----SSQDPSILQROESSVRLMKTLALVPGPATATILFPI 259
 DB 453 ALFQHLTCVPIILDSLLTLAGIINEQBDVYKQKOTSLQARELIDILVKGNIATV-- 510
 QY 260 RKVOYRORRLRLKQK-----QEEFQHEAOLLSRAKPEDRESLSKACVCLSSF 309
 DB 511 -RNSLOEAAVLYEHLFVQODIKITPTEDVDLVPVEQLRRLPEER-----TKVCMDKE 564
 QY 310 KSCVPLEGCHVSCTECYRALPEPKKCPICROAITEVPIPLVNS 352
 DB 565 VGVIFPCGHLVYCKDC--APSLRCKPICRSITIKGVTRFIS 604

RESULT 6
 T32659
 hypothetical protein K11D12.9 - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C:Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
 C:Accession: T32659
 R:Henkhaus, J.; Wohldmann, P.; Gilliam, B.
 submitted to the EMBL Data Library, December 1997
 A:Description: The sequence of C. elegans cosmid K11D12.
 A:Reference number: Z21207
 A:Accession: T32659
 A:Status: preliminary; translated from GB/EMBL/DDBJ
 A:Molecule type: DNA
 A:Residues: 1-316 <HEN>
 A:Cross-references: UNIPROT:Q44624; UNIPARC:UPI000017B4D; EMBL:AF039047; PIDN:AAB94229.
 A:Experimental source: strain Bristol N2; clone K11D12
 C:Genetics:
 A:Gene: CSP:K11D12.9
 A:Map position: 5
 A:Introns: 21/2; 55/3; 110/3; 184/3; 221/3

Query Match 7.5%; Score 136.5; DB 2; Length 316;
 Best Local Similarity 20.4%; Pred. No. 0.0081;
 Matches 75; Conservative 54; Mismatches 120; Indels 119; Gaps 14;
 QY 21 VTAAVSVYRKARVSOELKGAKV-----HLGEDLKSILSEAPKCVPAVAVIGAVNS 74
 DB 29 IYRLATLREKERDRKVDVDSFTILKNRINHLNKEKQCLSE-----VGE 74
 QY 75 VKETL--NQGFVNCGVIOQLTLQHKVMWMTTLMDSCKIHQRTVYVDFDLVPH 132
 DB 75 LKRLLEDSBDLDKDCDKNRILM-----E 98
 QY 133 DGVDAVVRVLPKPLDSVDLGLETYEEKFHPISIGFTDVIIGHYISGRPKGIQTEEMLVKYG 192

DB 99 KEVERA-----DALDKLTIGNRQOEIHQKE-----LSHRKKIYSEKARK-- 142
 QY 193 ATLTVGELVLDNNSVRLQPKQMOYLLSSQDPSSLQRO-----ESSVRLMKYLA 244
 DB 143 -----DEELINIQKQKTIVEMELERR--SNLDEQNTNVRMEKSKYQL-KPLV 188
 QY 245 LVFGPATCATLFFILRKQYLRQERLRL--KOMQEF-----OEHA 284
 DB 189 LDELITKHSQLVLDLSTEFLLPNINAVKMLYKELFESFQLETNVAESKLSMERREVEE 248
 QY 285 QLSRAKPEDR--ESLSKACVCLSSFKSCVPLEGCHVSCTECYRALPEPKKCPICROA 342
 DB 249 QLSRNRBPQRQELTVLAECCICLATKPSIYVMPRLHITGCGYDA--SDPRECPTRST 307
 QY 343 ITRVPLV 350
 DB 308 IENSIYV 315

RESULT 7
 T48167
 hypothetical protein T1008.160 - Arabidopsis thaliana
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C:Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 09-Jul-2004
 C:Accession: T48167
 R:Bevan, M.; Pohl, T.; Weizenegger, T.; Bancroft, I.; Mewes, H.W.; Lemcke, K.; Mayer, K
 submitted to the Protein Sequence Database, March 2000
 A:Reference number: Z24486
 A:Accession: T48167
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-428 <BEV>
 A:Cross-references: UNIPROT:Q9M029; UNIPARC:UPI000004A939; EMBL:AL161746
 A:Experimental source: cultivar Columbia; BAC clone T1008
 C:Genetics:
 A:Map position: 5
 A:Introns: 85/2; 100/3; 142/3; 174/1; 203/2; 229/3; 278/3; 303/1; 404/2
 A:Note: T1008.160

Query Match 7.3%; Score 134.5; DB 2; Length 428;
 Best Local Similarity 18.0%; Pred. No. 0.017;
 Matches 47; Conservative 42; Mismatches 105; Indels 67; Gaps 6;

QY 151 GLFTVYEFKHPISIGFTDVIIGHYISGRPKGIQTEEMLVKGAATLVGVGLVLDNNSVRL 210
 DB 174 GVDGLSEWQDPTDRDITLSMHIISGKCPSGYIE--QDITKSSYYVAVGVYLVNEVKATI 232
 QY 211 QPPKQMOYLLSSQDPSILQROESSVRL----- 239
 DB 233 DIQEGVLYDTITNAVYNGSPNDKCTLSVPLFGTNAAVLTSPGPKLANSKNEFCALSTE 292
 QY 240 --WKVIALVFGPATCATLFFILRKQYLRQERLRLKOMQEFQHE----- 283
 DB 293 PMIIVYICMGVLT--ALLIIVSLFNKRQPYTE---DETVDNDVAVPLIGKDDNS 346
 QY 284 -----AQLSRAKPEDRESLSKACVCLSSFKSCVPLEGCHVSCTECYRALP 331
 DB 347 SWCSSYSLTSTEBEGHGHGHSSTRYLCAICYDAPRDCFFLSGHCIVACFOGTRIA 406
 QY 332 EPKK-CPICROAITEVPIPLVNS 351
 DB 407 ETSGEFCVCKKIRVKKIIN 427

RESULT 8
 JCS964
 apoptosis inhibitor - pig
 C:Species: Sus scrofa domestica (domestic pig)
 C:Date: 04-Sep-1998 #sequence_revision 04-Sep-1998 #text_change 09-Jul-2004
 C:Accession: JCS964
 R:Stehlik, C.; de Martin, R.; Binder, B.R.; Lipp, J.
 Biochem. Biophys. Res. Commun. 243, 827-832, 1998

A/Title: Cytokine induced expression of porcine inhibitor of apoptosis protein (Iap) Iap
 A/Reference number: JCS964; MUID:98162622; PMID:9501011
 A/Accession: JCS964
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-358 <STE>
 A/Cross-references: UNIPROT:062640; UNIPARC:UPI000031A8D; GB:U79142; NID:92957174; PIND: F307-351/Domain: RING finger homology <RNG>

Query Match 7.2%; Score 131.5; DB 2; Length 358;
 Best Local Similarity 25.5%; Pred. No. 0.023;
 Matches 35; Conservative 30; Mismatches 61; Indels 11; Gaps 4;

221 LSSQDPDILQROESSVRLMKVLAIVFGFATCATLFFILRKQYLRQERLTKQM--QEE 278
 Db ISEQHDVYKQKTQSTLARELIDILVKNVATIF---KNSIQEIDPMYKFLFYQOD 284
 QY 279 FQENHAQLSRAPED--RESLSACVCLSSFRKCVFLECGHVCCTECYRALPPPK 335
 Db 285 IKYLPTEWVSDLSMEBQLRLQERTCKVCMDEKVSIVFIPCGHLVVCNDC---APSLRK 341
 QY 336 CPICROATRVYPIVNS 352
 Db 342 CPICRGITKGVTRPLS 358

RESULT 9

68824
 rngb protein, cytosolic - slime mold (Dictyostelium discoideum)
 N/Alternate names: RING finger protein
 C/Species: Dictyostelium discoideum
 C/Date: 04-Dec-1997 #sequence_revision 12-Dec-1997 #text_change 09-Jul-2004
 C/Accession: S68824
 R/Kawata, T.; Steel, J.B.; Williams, J.G.
 FEBS Lett. 386, 103-109, 1996
 A/Title: RINGB: a Dictyostelium RING finger protein that is specifically located in mature
 A/Reference number: S68824; MUID:96228044; PMID:8647262
 A/Accession: S68824
 A/Molecule type: mRNA
 A/Residues: 1-943 <KAM>
 A/Cross-references: UNIPROT:Q7M3S9; UNIPARC:UPI000017B18C
 A/Experimental source: maturing cells
 C/Genetics:
 A/Gene: rngb
 C/Keywords: zinc
 F:893-937/Domain: RING finger homology <RNG>

Query Match 7.1%; Score 130; DB 2; Length 943;
 Best Local Similarity 19.0%; Pred. No. 0.1; Mismatches 133; Indels 102; Gaps 15;
 Matches 72; Conservative 71; Mismatches 133; Indels 102; Gaps 15;

19 SVVTAALSYVRQKARVS---QELKAKKVLGDLKSLSEAPGKCVPAVIEGAVR 73
 Db 621 SLITNOIQSIIODELTLKKEYSELKKHSLYSEDIDLPET---CLKLEBTH-VK 675
 QY 74 SVKETLNSQFVENCQVIGRLTLOEHKMWNRRTTHLMNDCSKIHQRTVTPDLPV 130
 Db 676 SLKLR---VKGLPSSNQSLTQQ-QIPQOPTTITCN-SQTIQQO-----PLPPIQQ 723
 QY 131 -----HEDGVDAVAVLKLPSVDLGLFTYVEKHPISQSFPTDVIYHIGSERPK 180
 Db 724 QQQQQQQQQQQQQQQQPEIQQLMLQLQLSQSQSQQQQNDID-----KQKQKE 773
 QY 181 GIGETEMLKVGATLTGVEGLVDNNSVRLQPPKQMQYLLSSQ-----KQKQKE 773
 Db 774 KIQQEQQQQ---LKNIRLSSISNSSTLSSD---SFYFSKIQELSNQKQQAAT 826
 QY 225 DFDLSLQROESSVRLMKVLAIVGFATCATLFFILRKQYLRQERLTKQMEEF----- 279
 Db 827 DRNKKIKDENQNKTKLG-----LSDMDHYQLLELSSPHNGIK 867
 QY 280 -----QEHQAQLSRAPEDRESLSACVCLSSFRKCVFLECGHVCCTECYRALPE 332

Db 868 QIGSIKDRYLNRLVELKEKDQLKQNSCVIACSNPNVILLPCHSSLCSDCCSKL-- 925
 QY 333 PKKCPICROATRVPIPLY 350
 Db 926 -TKCPICRSHIENKISIT 942

RESULT 10

A96664
 Unknown protein T12P18.9 [imported] - Arabidopsis thaliana
 C/Species: Arabidopsis thaliana (mouse-ear cress)
 C/Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
 C/Accession: A96664
 R/Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, C.M.; Chung, M.K.; Comn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Hultzer, L.
 Nature 408, 816-820, 2000
 A/Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marzella, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
 A/Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
 A/Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
 A/Reference number: A96141; MUID:21016719; PMID:11130712
 A/Accession: A96664
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-200 <STO>
 A/Cross-references: UNIPROT:Q9CAK2; UNIPARC:UPI0000A5051; GB:AE005173; NID:96358784; PIND: A96664
 A/Genetics:
 A/Gene: T12P18.9
 A/Map position: 1

Query Match 6.8%; Score 124.5; DB 2; Length 200;
 Best Local Similarity 28.0%; Pred. No. 0.036;
 Matches 52; Conservative 31; Mismatches 94; Indels 9; Gaps 6;

17 TTSVTAALSYVRQKARVSQELKAKKVLGDLKSLSEAPGKCVPAVIEGAVRSV 75
 Db 8 TCCSAAALVYLIGSSGDAVLETVTRVQNLKEALTL-ELDSKILPFTVAVNSGRVGS- 65
 QY 76 KETLNSQFVENCQVIGRLTLOEHKMWNRRTTHLMNDCSKIHQRTVTPDLPVHBDG 135
 Db 66 -ETPIKCHSGIRGVIVETAEQHFLEKHNKNGS-WQDSALMSMSKXEPWFL--DDGT 120
 QY 136 DVAVRVLKPLSDVLDGLFTYVEKHPISQSFPTDVIYHIGSERPKGIQETEMLKVGATL 195
 Db 121 S-RVHWGARGATGPFALTVGSEVFEESGRSIVRTGLDLOGLKMLGVKRIERVLPTGIPL 179
 QY 196 TGVGEL 201
 Db 180 TIVGEV 185

RESULT 11

A45679
 Inhibitor-of-apoptosis polypeptide (IAP) - Cydia pomonella granulosis virus CpGV
 C/Species: Cydia pomonella granulosis virus CpGV
 C/Date: 21-Sep-1993 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
 C/Accession: A45679
 R/Crook, N.B.; Clem, R.V.; Miller, L.K.
 J. Virol. 67, 2168-2174, 1993
 A/Title: An apoptosis-inhibiting baculovirus gene with a zinc finger-like motif.
 A/Reference number: A45679; MUID:93188168; PMID:8445726
 A/Accession: A45679
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-275 <CRO>
 A/Cross-references: UNIPROT:P41436; UNIPARC:UPI000012D0CB; GB:L05494; NID:9289583; PIND: C/Note: sequence extracted from NCBI backbone (NCBIN:127014, NCBIR:127015)
 C/Superfamily: viral apoptosis inhibitor IAP; RING finger homology

Query Match 6.7%; Score 123; DB 2; Length 275;

Best Local Similarity 22.8%; Pred. No. 0.07;
Matches 44; Conservative 30; Mismatches 55; Indels 64; Gaps 9;

QY 183 QTEEMKATGATLTGCVGLVLDNNVRLPPKQMOYIIS--QDFSLROQSSVRLM 240

DB 124 QPEQWADGPFYTG---DNTKC-----FYCDGGIKQMEPDVMEQHR-W 168

QY 241 KYLALVFGATCATLFFILRKQYLR-----QERLKKQOESEF 279

DB 169 -----PDRCAVYVLVGRDYVQVITBEACVLPGEENTVTAPVSEPIPETKLESP 220

QY 280 QEHKQLLSRAKPEDEBSLKSACVVCISSEKSCVPLECGHVCSTECYRALPEPKKCPIC 339

DB 221 QVEDSLCKICVYEE-----CIYC-----FPGCHVAVCAKCALSTV---DKCPMC 262

QY 340 ROATRVVPLVNS 352

DB 263 RKIVTSVLKVPFS 275

RESULT 12

T01251
hypothetical protein Atg38190 [imported] - Arabidopsis thaliana

N:Alternate names: hypothetical protein F16M14.12

C:Species: Arabidopsis thaliana (mouse-ear cress)

C:Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 09-Jul-2004

R:Roundley, S.D.; Kaul, S.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes, submitted to the EMBL Data Library, July 1998

A:Description: Arabidopsis thaliana chromosome II BAC F16M14 genomic sequence.

A:Reference number: Z14213

A:Accession: T01251

A:Status: translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-124 <ROU>

A:Cross-references: UNIPROT:O80444; UNIPARC:UP100000A85FB; EMBL:AC003028; NID:g3335356;

A:Experimental source: cultivar Columbia

R:Lin, X.; Kaul, S.; Roundley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.; euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Frazer, C.M.; Venter, J. Nature 402, 761-768, 1999

A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.

A:Reference number: A84420; MUID:20083487; PMID:10617197

A:Accession: A84802

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-124 <STO>

A:Cross-references: UNIPARC:UP100000A85FB; GB:AE002093; NID:g3335367; PIDN:AAC27168.1; C

C:Genetics:

A:Gene: Atg38190; F16M14.12

A:Map position: 2

A:introns: 100/2

Query Match 6.6%; Score 121.5; DB 2; Length 124;

Best Local Similarity 32.0%; Pred. No. 0.032;

Matches 24; Conservative 13; Mismatches 29; Indels 9; Gaps 2;

QY 277 EEFQHEAQLLSRAKPEDEBSLKSACVVCISSEKSCVPLECGHVCSTECYRALPEPKK-K 335

DB 56 EEFMGNDGASNR-----RRLCAICFDVPRDCFLPCGHVSVCYCGCTMGADSDS 107

QY 336 CPICRQATRVVPLV 350

DB 108 CPICRKRKKVKRY 122

RESULT 13

D36828
orf13 protein - Autographa californica nuclear polyhedrosis virus

C:Species: Autographa californica nuclear polyhedrosis virus, AcMNPV

C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004

C:Accession: D36828; C72853

R:Braunagel, S.C.; Daniel, K.D.; Reilly, L.M.; Guarino, L.A.; Hong, T.; Summers, M.D.

Virology 191, 1003-1008, 1992

A:Title: Sequence, genomic organization of the EcoRI-A fragment of Autographa californica

VP8 of rotavirus. A:Reference number: A44221; MUID:93079853; PMID:1333113

A:Accession: D36828

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-286 <BRA>

A:Cross-references: UNIPROT:P41435; UNIPARC:UP10000178P99; GB:S52569

R:Hayes, M.D.; Howard, S.C.; Kuzio, J.; Lopez-Ferber, M.; Possee, R.D.

Virology 202, 586-605, 1994

A:Title: The complete DNA sequence of Autographa californica nuclear polyhedrosis virus.

A:Reference number: A72850; MUID:94303173; PMID:8030224

A:Accession: C72853

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-199, 'L', 201-286 <AVR>

A:Cross-references: UNIPARC:UP1000012D0B8; GB:L22858; NID:9510708; PIDN:AAA6657.1; PID:

C:Genetics:

A:Gene: Ac-1AP1

C:Superfamily: viral apoptosis inhibitor IAP; RING finger homology

Query Match 6.4%; Score 118; DB 2; Length 286;

Best Local Similarity 40.4%; Pred. No. 0.18;

Matches 21; Conservative 7; Mismatches 22; Indels 2; Gaps 1;

QY 299 KSACVCLSSFFKSCVPLECGHVCSTECYRALPEPKKCPICRQATRVVPLV 350

DB 235 KYECVCLERQDAVLMPCRHFCVVCOCYFGIDQ--KCPTRQDVTFIKIF 284

RESULT 14

T41772

IAP1 orf27 - Bombyx mori nuclear polyhedrosis virus (isolate T3)

C:Species: Bombyx mori nuclear polyhedrosis virus, BmSNV

A:Variety: isolate T3

C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004

C:Accession: T41772

R:Gomi, S.; Majima, K.; Maeda, S.

J. Gen. Virol. 80, 1323-1337, 1999

A:Title: Sequence analysis of the genome of Bombyx mori nucleopolyhedrovirus.

A:Reference number: Z22020; MUID:99281911; PMID:10355780

A:Accession: T41772

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-292 <KAM>

A:Cross-references: UNIPROT:O92394; UNIPARC:UP100000F314F; EMBL:L33180; NID:g3745835; PI

A:Experimental source: isolate T3

C:Genetics:

A:Note: iap1

C:Superfamily: viral apoptosis inhibitor IAP; RING finger homology

Query Match 6.4%; Score 118; DB 2; Length 292;

Best Local Similarity 40.4%; Pred. No. 0.18;

Matches 21; Conservative 7; Mismatches 22; Indels 2; Gaps 1;

QY 299 KSACVCLSSFFKSCVPLECGHVCSTECYRALPEPKKCPICRQATRVVPLV 350

DB 241 KYECVCLERQDAVLMPCRHFCVVCOCYFGIDQ--KCPTRQDVTFIKIF 290

RESULT 15

T16028

hypothetical protein F10D7.5 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 02-Aug-2002

C:Accession: T16028

R:Raich, A.

submitted to the EMBL Data Library, November 1995

A:Description: The sequence of C. elegans cosmid F10D7.

A:Reference number: Z18448

A:Accession: T16028

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA
A:Residues: 1-824 <TAI>
A:Cross-references: UNIPARC:UPI00001797E7; EMBL:U40945; NID:G1072208; PID:G1072213; PIDN
C:Gene: CESP:F10D7.5
A:Introns: 83/1; 108/1; 136/2; 174/1; 217/1; 236/2; 278/2; 325/3; 354/3; 384/1; 399/3; 4
C:Superfamily: fruit fly finger protein neutralized; RING finger homology
F/769-817/Domain: RING finger homology <RRN>
Query Match 6.4%; Score 117.5; DB 2; Length 824;
Best Local Similarity 34.7%; Pred. No. 0.77;
Matches 26; Conservative 7; Mismatches 35; Indels 7; Gaps 2;
QY 279 FOEHAQLSRKPEDRESLSKACVVCISFHSKCVLECGHVCSCTECVRALPEPK-KCP 337
Db 756 FQRTGNGAQGVNKGDE-----CTTCMDAPVNSVLYTCGHMCWCFECGRRLLTTKGTCP 809
QY 338 ICROAITRVIPLYNS 352
Db 810 ICRAPVQDVIKTYKS 824

Search completed: February 24, 2006, 08:30:08
Job time : 43 secs

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: February 24, 2006, 08:22:04 ; Search time 188 Seconds
(without alignments)
822.667 Million cell updates/sec

Title: US-09-978-360A-437

Perfect score: 1831
Sequence: 1 MESGRPSLQFILGTSV.....PKKPCICQALTRVPLVNS 352

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq.21:.*
1: geneeqp1980s:.*
2: geneeqp1990s:.*
3: geneeqp2000s:.*
4: geneeqp2001s:.*
5: geneeqp2002s:.*
6: geneeqp2003as:.*
7: geneeqp2003bs:.*
8: geneeqp2004s:.*
9: geneeqp2005s:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1831	100.0	352	3 AAB25794	AAB25794 Human sec
2	1831	100.0	352	4 AAE06602	AAE06602 Human pro
3	1831	100.0	352	4 AAB50174	AAB50174 Human tra
4	1831	100.0	352	4 AAB75380	AAB75380 Human sec
5	1831	100.0	352	5 AAB61461	AAB61461 Human NF-
6	1831	100.0	352	5 AAB97404	AAB97404 Novel hum
7	1831	100.0	352	8 ADP19181	ADP19181 Human sec
8	1831	100.0	352	8 ADR89550	ADR89550 Apoptosis
9	1826	99.7	392	6 AAU15848	AAU15848 Human nov
10	1826	99.7	392	6 ABUS4917	ABUS4917 Human nov
11	1824	99.6	352	5 ABP61460	ABP61460 Human NF-
12	1818	99.3	352	4 AAB94353	AAB94353 Human pro
13	1795	98.0	511	8 ADU02286	ADU02286 Novel hum
14	1328.5	72.6	263	6 ABJ38698	ABJ38698 Human nuc
15	901	49.2	174	4 AAU16309	AAU16309 Human nov
16	901	49.2	174	6 ABUS5378	ABUS5378 Human nov
17	854	46.6	165	5 ABB90304	ABB90304 Human pol
18	445	24.3	91	2 AAU13137	AAU13137 Human sec
19	442.5	24.2	338	4 AAB57873	AAB57873 Drosophil
20	439	24.0	90	2 AAU11645	AAU11645 Human 5'
21	437	23.9	88	2 AAU11871	AAU11871 Human 5'
22	267.5	14.6	338	8 ADT56108	ADT56108 Plant pol
23	252.5	13.8	375	8 ADT60537	ADT60537 Plant pol
24	231	12.6	232	8 ADX78340	ADX78340 Plant ful

25	201	11.0	383	3 AAG32339	AAG32339 Arabidops
26	200	10.9	383	3 AAG10096	AAG10096 Arabidops
27	200	10.9	399	3 AAG10095	AAG10095 Arabidops
28	188.5	10.3	332	7 ADD25209	ADD25209 Fertilily
29	188.5	10.3	332	8 ADN61224	ADN61224 Radish nu
30	187.5	10.2	242	3 AAG32340	AAG32340 Arabidops
31	186.5	10.2	242	3 AAG10097	AAG10097 Arabidops
32	184.5	10.1	163	8 ADY09490	ADY09490 Plant ful
33	183	10.0	235	8 ADX67603	ADX67603 Plant ful
34	177	9.7	206	3 AAG32341	AAG32341 Arabidops
35	172	9.4	366	8 ADT57025	ADT57025 Plant pol
36	163	8.9	357	4 AAE10909	AAE10909 Human apo
37	163	8.9	372	3 AAY56882	AAY56882 Human gen
38	163	8.9	403	7 AEM85233	ABM85233 Human pro
39	155.5	8.5	234	6 ADY52508	ADY52508 Human Tsg
40	155.5	8.5	303	6 ADA54907	ADA54907 Human pro
41	155.5	8.5	696	6 ADA54857	ADA54857 Human pro
42	155.5	8.5	723	3 AAY96308	AAY96308 Human RIN
43	155.5	8.5	723	5 ABG32886	ABG32886 Human RIN
44	155.5	8.5	723	7 ADB64418	ADB64418 Human pro
45	155.5	8.5	723	9 ADY52503	ADY52503 Human Tsg

ALIGNMENTS

RESULT 1	AAB25794	standard; protein, 352 AA.
ID	AAB25794	standard; protein, 352 AA.
AC	AAB25794;	
DT	28-NOV-2000	(first entry)
DE	Human secreted protein SEQ ID #106.	
KW	Human; secreted protein; forensic procedure; gene therapy;	
KW	chromosome mapping; cancer; autoimmune disease; cardiovascular disorder;	
KW	cystic fibrosis; hypothyroidism; immunological disorder; amyloidosis;	
KW	brain disorder; skeletal muscle disorder; eye disorder; obesity;	
KW	mitochondriocytopathy; diabetes; atherosclerosis; Alzheimer's disease;	
KW	neurodegenerative disorder; graft rejection; dementia; hyperlipidaemia;	
KW	septic shock; impotence.	
OS	Homo sapiens.	
PN	WO200037491-A2.	
PD	29-JUN-2000.	
XX	20-DEC-1999;	99WO-IB002058.
XX	22-DEC-1998;	98US-0113686P.
XX	25-JUN-1999;	99US-0141032P.
XX	(GSET) GENSET.	
XX	Bougueleret L, Dumas J, Duclert A;	
XX	WPI: 2000-442637/38.	
XX	N-PSDB; AAA87756.	
XX	Polynucleotides and polypeptides encoding proteins with signal peptides,	
XX	useful in diagnostic, forensic, gene therapy and chromosome mapping	
XX	procedures.	
XX	Claim 9; Page 279-280; 306pp; English.	
CC	This sequence represents a human secreted protein amino acid sequence.	
CC	The invention relates to sequences AAB25794-AB2774 which encode human	
CC	secreted proteins AAB25763-B25812. The proteins include signal peptides.	
CC	included in the invention are a host cell containing one of the cDNA	
CC	sequences, and a purified antibody capable of binding to one of the	

secreted proteins. Also contained in the invention are methods for storing the sequence data on a computer system, and a method for identifying features of the cDNA sequences using a computer programme. The cDNAs are useful for expressing secreted proteins or fragments to obtain antibodies capable of specifically binding to the secreted proteins. The cDNAs may also be useful in diagnostic, forensic, gene therapy and chromosome mapping procedures and may be used to design expression vectors and secretion vectors. The proteins of the invention may be used to treat diseases including cancer, autoimmune diseases, cardiovascular disorders, cystic fibrosis, hypothyroidism, immunological disorders, amyloidosis, brain disorders, skeletal muscle disorders, eye disorders, obesity, mitochondrial cytopathies, diabetes, atherosclerosis, neurodegenerative disorders, graft rejection, Alzheimer's disease, dementia, hyperlipidaemia, septic shock and impotence.

Sequence 352 AA;

Query Match 100.0%; Score 1831; DB 3; Length 352;
Best Local Similarity 100.0%; Pred. No. 1.4e-168;
Matches 352; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MESSGRPSLCOFILGTTSVTAAVYRQKARVSOELGAKKXVHIGEDLKSILSEAPG 60
DB 1 MESSGRPSLCOFILGTTSVTAAVYRQKARVSOELGAKKXVHIGEDLKSILSEAPG 60
QY 61 KCVPAVIEGAVRSVKETLNSQFVENCXGVIOQLTLOEHKVMNRTHLMNDSKIIHOR 120
DB 61 KCVPAVIEGAVRSVKETLNSQFVENCXGVIOQLTLOEHKVMNRTHLMNDSKIIHOR 120
QY 121 TNNVPEFLVPHEDGDVAVRVLKPLDSVDGLFTVYEKFPHSIQSFVDVIGHYISGERPK 180
DB 121 TNNVPEFLVPHEDGDVAVRVLKPLDSVDGLFTVYEKFPHSIQSFVDVIGHYISGERPK 180
QY 181 GIOETHEMLKVGATLTGGEVLVDNNSVRLQPPKQGYIYSSODPSSLQROESSVRLW 240
DB 181 GIOETHEMLKVGATLTGGEVLVDNNSVRLQPPKQGYIYSSODPSSLQROESSVRLW 240
QY 241 KVTALVGFATCATLFFILRKQYIQRQERLRLKMOEFQEHBAQLLSRAKPEDRESLKS 300
DB 241 KVTALVGFATCATLFFILRKQYIQRQERLRLKMOEFQEHBAQLLSRAKPEDRESLKS 300
QY 301 ACVCLSSFKSCVFLGCGHVCSTECYRALPEPKKPCICQATIRVILPLVNS 352
DB 301 ACVCLSSFKSCVFLGCGHVCSTECYRALPEPKKPCICQATIRVILPLVNS 352

RESULT 2

AAE06602 ID AAE06602 standard; protein; 352 AA.

AC AAE06602;

XX 25-SEP-2001 (first entry)

DE Human protein having hydrophobic domain, HP10649.

XX Human; hydrophobic domain; gene therapy; nutritional supplement;
KW cell proliferation; immunomodulatory; autoimmune disorder; antimicrobial;
KW multiple sclerosis; rheumatoid arthritis; insulin-dependent diabetes;
KW haemotopoiesis; tissue growth activity; Parkinson's disease; cystostatic;
KW Huntington's disease; Alzheimer's disease; chemotactic; chemokinetic;
KW haemostatic; thrombolytic; tumour growth inhibitor; anabolic;
KW contraceptive; antinfertility; antiinflammatory.

OS Homo sapiens.

XX MO200149728-A2.

XX 12-JUL-2001.

PD 28-DEC-2000; 2000MO-JP009359.

XX 06-JAN-2000; 2000JP-00000585.

PR 06-JAN-2000; 2000JP-00000585.
PR 11-JAN-2000; 2000JP-00002299.
PR 03-FEB-2000; 2000JP-00026862.
PR 03-MAR-2000; 2000JP-00058367.

PA (PROT-) PROTEGENE INC.
(SAGA) SAGAMI CHEM RES CENT.

PI Kato S, Kimura T;

DR MPI; 2001-418355/44.

DR N-PSDB; AAD12597.

PT Human proteins with hydrophobic domains and the nucleic acids encoding
them, useful for preventing diagnosing and treating e.g. cancer,
Alzheimer's and inflammation.

XX Claim 1, Page 122; 563pp; English.

The present sequence is human protein with hydrophobic domain, HP10649.
The polynucleotide and polypeptide of the invention may be used in the
prevention, diagnosis and treatment of diseases associated with
inappropriate polypeptide expression. The polynucleotides may be used to
produce the polypeptide, by inserting the nucleic acids into a host cell
and culturing the cell to express the protein. The polynucleotides and
its complementary sequences may also be used as DNA probes in diagnostic
assays and also used in gene therapy. The polypeptides may also be used
as antigens in the production of antibodies and in assays to identify
modulators of polypeptide expression and activity. The polypeptides and
nucleic acids may be used as nutritional supplements, to modulate
cytokine and cell proliferation activity, to modulate immune stimulation
or suppression (e.g. for the treatment of microbial infections and
autoimmune disorders such as multiple sclerosis, rheumatoid arthritis and
insulin-dependent diabetes), to modulate haematopoiesis, to modulate
tissue growth activity (e.g. for the treatment of Parkinson's disease,
Huntington's disease and Alzheimer's disease), to modulate actvlin and
inhibin activity (e.g. for controlling fertility), to modulate
chemotactic and chemokinetic activity, to modulate haemostatic and
thrombolytic activity, to modulate receptor ligand activity, to modulate
inflammation and to inhibit tumour growth

XX Sequence 352 AA;

Query Match 100.0%; Score 1831; DB 4; Length 352;
Best Local Similarity 100.0%; Pred. No. 1.4e-168;
Matches 352; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MESSGRPSLCOFILGTTSVTAAVYRQKARVSOELGAKKXVHIGEDLKSILSEAPG 60

DB 1 MESSGRPSLCOFILGTTSVTAAVYRQKARVSOELGAKKXVHIGEDLKSILSEAPG 60

QY 61 KCVPAVIEGAVRSVKETLNSQFVENCXGVIOQLTLOEHKVMNRTHLMNDSKIIHOR 120

DB 61 KCVPAVIEGAVRSVKETLNSQFVENCXGVIOQLTLOEHKVMNRTHLMNDSKIIHOR 120

QY 121 TNNVPEFLVPHEDGDVAVRVLKPLDSVDGLFTVYEKFPHSIQSFVDVIGHYISGERPK 180

DB 121 TNNVPEFLVPHEDGDVAVRVLKPLDSVDGLFTVYEKFPHSIQSFVDVIGHYISGERPK 180

QY 181 GIOETHEMLKVGATLTGGEVLVDNNSVRLQPPKQGYIYSSODPSSLQROESSVRLW 240

DB 181 GIOETHEMLKVGATLTGGEVLVDNNSVRLQPPKQGYIYSSODPSSLQROESSVRLW 240

QY 241 KVTALVGFATCATLFFILRKQYIQRQERLRLKMOEFQEHBAQLLSRAKPEDRESLKS 300

DB 241 KVTALVGFATCATLFFILRKQYIQRQERLRLKMOEFQEHBAQLLSRAKPEDRESLKS 300

QY 301 ACVCLSSFKSCVFLGCGHVCSTECYRALPEPKKPCICQATIRVILPLVNS 352

DB 301 ACVCLSSFKSCVFLGCGHVCSTECYRALPEPKKPCICQATIRVILPLVNS 352

RESULT 3

ID	ABB50174
XX	ABBS0174 standard; protein; 352 AA.
AC	ABBS0174;
DT	05-FEB-2002 (first entry)
XX	
DE	Human transcription factor TRFX-25.
KM	Human; transcription factor; TRFX; cell proliferative disease;
KW	autoimmune disease; inflammation; neurological disease;
RV	developmental disorder; cancer; AIDS; infection; cytostatic; anti-HIV;
XX	neuroprotective; antiinflammatory; gene therapy.
OS	Homo sapiens.
PN	WO20017277-A2.
XX	
PD	04-OCT-2001.
PF	
PR	13-MAR-2001; 2001WO-US008117.
XX	
PA	13-MAR-2000; 2000US-0186986P.
PI	(INCY-) INCYTE GENOMICS INC.
P1	Hillman JT, Baughn MR, Yue H, Lal P, Lu DM, Patterson C, J;
XX	Azizmal Y, Bandman O, Tang YT, Machur P, Shah P, Au-Young J;
PT	Reddy R;
DR	MP1; 2001-570896/64.
N-PSDB;	ABR62998.
PT	Novel transcription factor polypeptides, used to treat diseases associated with altered activity and expression of TRFX, and to screen for agents capable of modulating its activity.
XX	
XX	Claim 1; Page 168-169; 327pp; English.
CC	The present sequence is the protein sequence for a human transcription factor. The transcription factor and its coding sequence are useful in the diagnosis, treatment and prevention of diseases associated with altered expression of the transcription factor e.g. cell proliferative, autoimmune/inflammatory, neurological and developmental disorders. A number of specific disorders/diseases are given in the specification, including: arteriosclerosis, cirrhosis, hepatitis, cancers, AIDS, allergies, anemia, asthma, autoimmune thyroiditis, bronchitis, atopic dermatitis, diabetes mellitus, emphysema, Goodpasture's syndrome, gout, Grave's disease, multiple sclerosis, osteoarthritis, pancreatitis, psoriasis, rheumatoid arthritis, systemic lupus erythematosus, ulcerative colitis, uveitis, Alzheimer's disease, Huntington's disease, Parkinson's disease, stroke, and viral, bacterial, fungal and protozoal infections
SO	Sequence 352 AA;
Query Match	100.0%; Score 1831; DB 4; Length 352;
Best Local Similarity	100.0%; Pred. No. 1.4e-169;
Matches 352;	Conservative 0; Mismatches 0; Indels 0; Gaps 0
DQ	1 MESGGRPSICQITLLIGTTSVTAAALYSYVRKARVSQELKAKKHLEBDLKSILSEAG 60
Db	1 MESGGRPSICQITLLIGTTSVTAAALYSYVRKARVSQELKAKKHLEBDLKSILSEAG 60
OY	61 KCVPAVIEGAARSVKETINSQFVENCKVIRLTLOEHKMWMNRTHLMNDSKI IHR 120
Db	61 KCVPAVIEGAARSVKETINSQFVENCKVIRLTLOEHKMWMNRTHLMNDSKI IHR 120
OY	121 TWTVPDIDVPHEDGVDAVAVRLKPLDSVDLGLETVEYKEKHPISIQSTFDVI GHYISGERPK 180
Db	121 TWTVPDIDVPHEDGVDAVAVRLKPLDSVDLGLETVEYKEKHPISIQSTFDVI GHYISGERPK 180
OY	181 GIQTEBNLTKVATLTTCGEVLVLDNNSVRLQPPKGMQYIISOPDSLQLQRESSVRLW 240

[illegible]

Db 241 KYIALVGFATCATLFFILRKQYLOREBRLKQMOEFQHEAQLLSRAKPEDRESLKS 300

QY 301 ACVVCLSSFKSCVFLFCGHVCSCTECYRALPEPKKCPICROAITRVIPLYNS 352
Db 301 ACVVCLSSFKSCVFLFCGHVCSCTECYRALPEPKKCPICROAITRVIPLYNS 352

RESULT 5

ABP61461 ID ABP61461 standard; protein; 352 AA.

AC ABP61461;

DT 30-SEP-2002 (first entry)

DE Human NF-kB activating protein SEQ ID NO 75.

XX Human; NF-kB; nuclear factor kappa B; mouse; antiinflammatory;
KW immunomodulator; cytosolic; antiinfective; osteopathic; noctropic;
KW neuroprotective; anti-HIV; autoimmune disease; cancer; infection;
KW bone disease; AIDS; neurodegenerative disease; ischaemic disorder.

OS Homo sapiens.

PN WO200253737-A1.

PD 11-JUN-2002.

PF 25-DEC-2001; 2001WO-JP011389.

PR 28-DEC-2000; 2000JP-00402288.

PR 26-MAR-2001; 2001JP-00088912.

PR 24-AUG-2001; 2001JP-00254018.

XX (ASAH) ASAH KASEI KOGYO KK.

PI Matsuda A, Honda G, Muramatsu S, Nagano Y;

DR WPI; 2002-583617/62.

XX N-PSDB; ABQ91949.

PT NF-approximatelykB activating gene and expressed protein, applicable in

PT diagnosis and screening inhibitors or promoters to control excessive

PT activation or inhibition for treating e.g. inflammations, autoimmune

PT diseases and cancer.

PS Claim 1; Page 349-352; 841pp; Japanese.

XX The invention relates to a purified protein (I), comprising one of 90

CC fully defined sequences (ABP61424-ABP61513) or a protein based on any of

CC the sequences but with some amino acids deleted, substituted or added and

CC with a NF-kB (nuclear factor kappa B) activating effect. The protein and

CC inhibiting gene (ABQ91912-ABQ92001) are useful in diagnosis and screening

CC inhibitors or promoters to control excessive activation or inhibition and

CC for treating e.g. inflammations, autoimmune diseases, cancers,

CC infections, bone diseases, AIDS, neurodegenerative diseases or ischaemic

XX disorders

XX Sequence 352 AA;

Query Match 100.0%; Score 1831; DB 5; Length 352;

Best Local Similarity 100.0%; Pred. No. 1.4e-168;

Matches 352; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MESGGRPSLCQFILLGTTSVVTAALYSVYRQKARVSOELKGAKKVLGEDIKSLISEAPG 60

Db 1 MESGGRPSLCQFILLGTTSVVTAALYSVYRQKARVSOELKGAKKVLGEDIKSLISEAPG 60

QY 61 KCVPAVAVICGAVSVKELTNSQFVENCCKGVICRLTLOEHKMWNRTHLMDCKSLIHOR 120

Db 61 KCVPAVAVICGAVSVKELTNSQFVENCCKGVICRLTLOEHKMWNRTHLMDCKSLIHOR 120

QY 121 TWTPFDLVPHEDGDVAVRVLKPLDSVDLGLFTYVKEFHPISIQSFPTDIGHYIGGERPK 180

Db 121 TWTPFDLVPHEDGDVAVRVLKPLDSVDLGLFTYVKEFHPISIQSFPTDIGHYIGGERPK 180

QY 181 GIQETEMKVGATLTGVEGLVDNNNSVRLQPKQGMQYLLSSQDPDSLQOESSVRLM 240

Db 181 GIQETEMKVGATLTGVEGLVDNNNSVRLQPKQGMQYLLSSQDPDSLQOESSVRLM 240

QY 241 KYIALVGFATCATLFFILRKQYLOREBRLKQMOEFQHEAQLLSRAKPEDRESLKS 300

Db 241 KYIALVGFATCATLFFILRKQYLOREBRLKQMOEFQHEAQLLSRAKPEDRESLKS 300

QY 301 ACVVCLSSFKSCVFLFCGHVCSCTECYRALPEPKKCPICROAITRVIPLYNS 352

Db 301 ACVVCLSSFKSCVFLFCGHVCSCTECYRALPEPKKCPICROAITRVIPLYNS 352

RESULT 6

ABB97404 ID ABB97404 standard; protein; 352 AA.

AC ABB97404;

DT 27-JUN-2002 (first entry)

DE Novel human protein SEQ ID NO: 672.

XX Human; antianaemic; vulnerary; antiinflammatory; immunomodulator;
KW antiinfectivity; cerebroprotective; cytosolic; rheumatic; gene therapy;
KW neuroprotective; antiparkinsonian; protein therapy; EST;
KW expressed sequence tag.

OS Homo sapiens.

PN WO200222660-A2.

PD 21-MAR-2002.

PF 10-SEP-2001; 2001WO-US026015.

PR 11-SEP-2000; 2000US-00659671.

XX (HYSE-) HYSEQ INC.

PI Tang YT, Liu C, Zhou P, Asundi V, Zhang J, Zhao QA, Ren F;

PI Xue AJ, Yang Y, Wehrman T, Drmanac R;

DR WPI; 2002-292408/33.

XX N-PSDB; ABN32590.

PT An isolated polynucleotide for treating diseases associated with its

PT encoded polypeptide such as cancer and multiple sclerosis.

PS Claim 20; SEQ ID NO 672; 509pp; English.

XX The present invention provides the protein and coding sequences of 444

CC novel human proteins. These were isolated from expressed sequences tags

CC (ESTs). They can be used to stimulate cell growth, to regulate

CC haematopoiesis e.g. to treat aplastic anaemia, to help tissue regrowth

CC e.g. in burn treatment, to regulate the immune system e.g. to treat

CC multiple sclerosis, to regulate activin or inhibin e.g. to treat

CC infertility, to regulate haemostasis or thrombolysis e.g. to treat stroke

CC and cancer, to screen for drugs, to treat inflammatory conditions e.g.

CC rheumatoid arthritis, and to treat nervous system disorders e.g.

CC Parkinson's disease. The present sequence is a protein of the invention

XX Sequence 352 AA;

Query Match 100.0%; Score 1831; DB 5; Length 352;

Best Local Similarity 100.0%; Pred. No. 1.4e-168;

Matches 352; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MESGGRPSLCQFILLGTTSVVTAALYSVYRQKARVSOELKGAKKVLGEDIKSLISEAPG 60

```

Db      1 MESSGRPSLCOFILIGTTSVVTALALYSYRQKARVSQELKGAKVHLGEDLSILSEAPG 60
Qy      61 KCPVAVIEGAVRSVKETLNSQFVENCCKVIOQLTLOEHKVMWNRTHLMDCKSIHOR 120
Db      61 KCPVAVIEGAVRSVKETLNSQFVENCCKVIOQLTLOEHKVMWNRTHLMDCKSIHOR 120
Qy      121 TWTVPFDLVPHEDGVDVAVRVLKPLDSVDLGLETVEYKEFHPSIOSFTDVIIGHYISGERPK 180
Db      121 TWTVPFDLVPHEDGVDVAVRVLKPLDSVDLGLETVEYKEFHPSIOSFTDVIIGHYISGERPK 180
Qy      181 GIOETEMLKVGATLTGVELVLDNNSVRLQPPKQGMQYLLSSODFDSLQROESSVRLM 240
Db      181 GIOETEMLKVGATLTGVELVLDNNSVRLQPPKQGMQYLLSSODFDSLQROESSVRLM 240
Qy      241 KTLALVFGFATCATLFFILRKQYLOQROERLRLKQOEFOEHEAQLSRAPKEDRESLSKS 300
Db      241 KTLALVFGFATCATLFFILRKQYLOQROERLRLKQOEFOEHEAQLSRAPKEDRESLSKS 300
Qy      301 ACVVCLSFKSCVPLECGHVCSCTECYRALPEPKKCPICROAITRVIPLYNS 352
Db      301 ACVVCLSFKSCVPLECGHVCSCTECYRALPEPKKCPICROAITRVIPLYNS 352

RESULT 7
ADP19181
ID      ADP19181 standard; protein; 352 AA.
XX
AC      ADP19181;
XX
DT      26-AUG-2004 (first entry)
XX
DE      Human secreted polypeptide #32.
XX
KW      Human; secreted protein; genetic disease.
XX
OS      Homo sapiens.
XX
PN      US2004110939-A1.
XX
PD      10-JUN-2004.
XX
PF      15-OCT-2001; 2001US-00978360.
XX
PR      17-DEC-1998; 98WO-IB002122.
XX
PR      09-FEB-1999; 99WO-IB000282.
XX
PR      21-JUN-2000; 2000WO-IB000951.
XX
PR      15-SEP-2000; 2000US-00663600.
XX
PA      (GEST ) GENSET SA.
PI      Dumas Milne Edwards J, Bougueleret L, Jobert S, Clusel C;
PI      Duclet A;
XX
DR      MPI: 2004-440404/41.
DR      N-PSDB; ADP18776.
XX
PT      New isolated polynucleotide encoding secreted polypeptide, useful for
PT      gene therapy, or in diagnostic procedures to identify individuals having
PT      genetic diseases resulting from abnormal expression of the genes.
XX
PS      Claim 2; SEQ ID NO 437; 113pp; English.
XX
CC      The invention relates to human cDNA sequences that encode human secreted
CC      proteins. The invention also relates to an antibody that specifically
CC      binds to a polypeptide of the invention and a method of binding the
CC      polypeptide to an antibody. The polynucleotides are useful for expressing
CC      the entire secreted proteins which they encode and for distinguishing
CC      human tissues and cells from non-human tissues and cells, and for
CC      distinguishing between human tissues and cells that do or do not express
CC      the polynucleotides comprising the cDNAs. The polynucleotides and
CC      polypeptides are useful in forensic procedures or diagnostic procedures
CC      to identify individuals with genetic diseases resulting from abnormal

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CC      expression of the genes corresponding to the cDNAs. The sequences are
CC      also useful in gene therapy to control or treat genetic diseases. This
CC      sequence represents a human secreted polypeptide of the invention. Note:
CC      The sequence data for this patent did not form part of the printed
CC      specification but was obtained in electronic format from USPTO at
CC      seqdata.uspto.gov/sequence.html.
XX
SQ      Sequence 352 AA;
XX
Query Match      100.0%; Score 1831; DB 8; Length 352;
Best Local Similarity 100.0%; Pred. No. 1,4e-168;
Matches 352; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 MESSGRPSLCOFILIGTTSVVTALALYSYRQKARVSQELKGAKVHLGEDLSILSEAPG 60
Db      1 MESSGRPSLCOFILIGTTSVVTALALYSYRQKARVSQELKGAKVHLGEDLSILSEAPG 60
Qy      61 KCPVAVIEGAVRSVKETLNSQFVENCCKVIOQLTLOEHKVMWNRTHLMDCKSIHOR 120
Db      61 KCPVAVIEGAVRSVKETLNSQFVENCCKVIOQLTLOEHKVMWNRTHLMDCKSIHOR 120
Qy      121 TWTVPFDLVPHEDGVDVAVRVLKPLDSVDLGLETVEYKEFHPSIOSFTDVIIGHYISGERPK 180
Db      121 TWTVPFDLVPHEDGVDVAVRVLKPLDSVDLGLETVEYKEFHPSIOSFTDVIIGHYISGERPK 180
Qy      181 GIOETEMLKVGATLTGVELVLDNNSVRLQPPKQGMQYLLSSODFDSLQROESSVRLM 240
Db      181 GIOETEMLKVGATLTGVELVLDNNSVRLQPPKQGMQYLLSSODFDSLQROESSVRLM 240
Qy      241 KTLALVFGFATCATLFFILRKQYLOQROERLRLKQOEFOEHEAQLSRAPKEDRESLSKS 300
Db      241 KTLALVFGFATCATLFFILRKQYLOQROERLRLKQOEFOEHEAQLSRAPKEDRESLSKS 300
Qy      301 ACVVCLSFKSCVPLECGHVCSCTECYRALPEPKKCPICROAITRVIPLYNS 352
Db      301 ACVVCLSFKSCVPLECGHVCSCTECYRALPEPKKCPICROAITRVIPLYNS 352

RESULT 8
ADR89550
ID      ADR89550 standard; protein; 352 AA.
XX
AC      ADR89550;
XX
DT      02-DEC-2004 (first entry)
XX
DE      Apoptosis-inducing protein, SEQ ID 74.
XX
KW      Cytostatic; Immunosuppressive; Neuroprotective; Vasotropic; Virucide;
KW      apoptosis; neurodegenerative disease; ischaemic disease; cancer;
KW      autoimmune disease; viral disease; human.
XX
OS      Homo sapiens.
XX
PN      WO2004078112-A2.
XX
PD      16-SEP-2004.
XX
PF      05-MAR-2004; 2004WO-JP002899.
XX
PR      07-MAR-2003; 2003JP-00061179.
PR      10-MAR-2003; 2003US-0452943P.
XX
PA      (ASAH-) ASAH KASEI PHARMA CORP.
PI      Muramatsu S, Takeda M, Matsuda A;
XX
DR      MPI: 2004-662343/64.
DR      N-PSDB; ADR89549.
XX
PT      New protein capable of inducing apoptosis, useful in screening for
PT      compounds that inhibit or induce apoptosis which may be used to treat
PT      neurodegenerative, ischemic, autoimmune and viral diseases, and cancer.

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XX Claim 1; SEQ ID NO 74; 316pp; English.
PS
XX
CC The present invention relates to novel purified proteins (1) and their
CC coding sequences (11) (ADRR9477-ADRR9550), which are capable of inducing
CC apoptosis. The proteins (1) are useful as a target in screening for
CC compounds that modulate apoptosis. Compounds that modulate the expression
CC or activity of the protein may be useful in treating neurodegenerative
CC diseases, ischemic diseases, cancer, autoimmune diseases, or viral
CC diseases. Measurement of the expression or activity of the protein may
CC also be used to diagnose or disease or a susceptibility to a disease.
XX
SQ Sequence 352 AA:
Query Match 100.0%; Score 1831; DB 8; Length 352;
Best Local Similarity 100.0%; Pred. No. 1.4e-168;
Matches 352; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MESGGRPSLCOFILGTTSTVTALYSVYRQKARVSOELKGAKKVHLGEDLKSTLSAPG 60
Db 1 MESGGRPSLCOFILGTTSTVTALYSVYRQKARVSOELKGAKKVHLGEDLKSTLSAPG 60
QY 61 KCVYVAVTEGAVRSVKETLSNQFVENCCKVYQRLTQEHKVMWNRTHLWDCSKIIHOR 120
Db 61 KCVYVAVTEGAVRSVKETLSNQFVENCCKVYQRLTQEHKVMWNRTHLWDCSKIIHOR 120
QY 121 TNTVPFDLPHEGDVAVRVYKPLDSVDGLFTVYKFKHPSIOSFTDVGHYISGRPK 180
Db 121 TNTVPFDLPHEGDVAVRVYKPLDSVDGLFTVYKFKHPSIOSFTDVGHYISGRPK 180
QY 121 TNTVPFDLPHEGDVAVRVYKPLDSVDGLFTVYKFKHPSIOSFTDVGHYISGRPK 180
Db 121 TNTVPFDLPHEGDVAVRVYKPLDSVDGLFTVYKFKHPSIOSFTDVGHYISGRPK 180
QY 181 GIQTEEMLKVGATLTGVEIYLDNNSVRLQPPKQMQVYLLSODPDSLQROESSVRLW 240
Db 181 GIQTEEMLKVGATLTGVEIYLDNNSVRLQPPKQMQVYLLSODPDSLQROESSVRLW 240
QY 241 KVALVGFATPCATLFFILRKQYIQROERLRLKMOEFQEHKQOLLSRAKPDRLSLNS 300
Db 241 KVALVGFATPCATLFFILRKQYIQROERLRLKMOEFQEHKQOLLSRAKPDRLSLNS 300
QY 301 ACVCLSSFFKSCVLECGHVCSTECYRALPEPKPCICQALTRVPLVNS 352
Db 301 ACVCLSSFFKSCVLECGHVCSTECYRALPEPKPCICQALTRVPLVNS 352
RESULT 9
AAU15848 ID AAU15848 standard; protein; 392 AA.
XX AC AAU15848;
XX
DT 07-NOV-2001 (first entry)
XX
XX Human novel secreted protein, Seq ID 801.
XX
XX Human; immunosuppressive; antiarthritic; antirheumatic; cytostatic;
KW cardiant; vasotrophic; cerebroprotective; neurotrophic; neuroprotective;
KW antibacterial; virocidic; fungicidal; ophthalmological; vulnary;
KW secreted protein; rheumatoid arthritis; hyperproliferative disorder;
KW cardiovascular disorder; cardiac arrest; cerebrovascular disorder;
KW cerebral ischaemia; angiogenesis; nervous system disorder;
KW Alzheimer's disease; infection; ocular disorder; corneal infection;
KW wound healing; epithelial cell proliferation; skin ageing; food additive;
KW preservative; antiproliferative.
XX
XX Homo sapiens.
XX
XX MO200155322-A2.
XX
XX PD 02-AUG-2001.
XX
XX PF 17-JAN-2001; 2001MO-US001341.
XX
XX PR 31-JAN-2000; 2000US-0179065P.
XX
XX PR 04-FEB-2000; 2000US-0180628P.
PR

PR 24-FEB-2000; 2000US-0184664P.
PR 02-MAR-2000; 2000US-0186350P.
PR 16-MAR-2000; 2000US-0189874P.
PR 17-MAR-2000; 2000US-0190076P.
PR 18-APR-2000; 2000US-0198123P.
PR 19-MAY-2000; 2000US-020515P.
PR 07-JUN-2000; 2000US-0209467P.
PR 28-JUN-2000; 2000US-0214886P.
PR 30-JUN-2000; 2000US-0215135P.
PR 07-JUL-2000; 2000US-0216647P.
PR 11-JUL-2000; 2000US-0216880P.
PR 11-JUL-2000; 2000US-0217496P.
PR 14-JUL-2000; 2000US-0218290P.
PR 26-JUL-2000; 2000US-0220963P.
PR 26-JUL-2000; 2000US-0220964P.
PR 14-AUG-2000; 2000US-0224518P.
PR 14-AUG-2000; 2000US-0224519P.
PR 14-AUG-2000; 2000US-0225213P.
PR 14-AUG-2000; 2000US-0225214P.
PR 14-AUG-2000; 2000US-0225266P.
PR 14-AUG-2000; 2000US-0225267P.
PR 14-AUG-2000; 2000US-0225268P.
PR 14-AUG-2000; 2000US-0225270P.
PR 14-AUG-2000; 2000US-0225447P.
PR 14-AUG-2000; 2000US-0225757P.
PR 14-AUG-2000; 2000US-0225758P.
PR 14-AUG-2000; 2000US-0225759P.
PR 18-AUG-2000; 2000US-0226279P.
PR 22-AUG-2000; 2000US-0226681P.
PR 22-AUG-2000; 2000US-0226682P.
PR 22-AUG-2000; 2000US-0227182P.
PR 23-AUG-2000; 2000US-0227009P.
PR 30-AUG-2000; 2000US-0228924P.
PR 01-SEP-2000; 2000US-0228287P.
PR 01-SEP-2000; 2000US-0229343P.
PR 01-SEP-2000; 2000US-0229344P.
PR 01-SEP-2000; 2000US-0229345P.
PR 05-SEP-2000; 2000US-0229509P.
PR 05-SEP-2000; 2000US-0229513P.
PR 06-SEP-2000; 2000US-0230437P.
PR 06-SEP-2000; 2000US-0230438P.
PR 08-SEP-2000; 2000US-0231242P.
PR 08-SEP-2000; 2000US-0231243P.
PR 08-SEP-2000; 2000US-0231244P.
PR 08-SEP-2000; 2000US-0231413P.
PR 08-SEP-2000; 2000US-0231414P.
PR 08-SEP-2000; 2000US-0232081P.
PR 08-SEP-2000; 2000US-0232081P.
PR 12-SEP-2000; 2000US-0231968P.
PR 14-SEP-2000; 2000US-0232397P.
PR 14-SEP-2000; 2000US-0232398P.
PR 14-SEP-2000; 2000US-0232399P.
PR 14-SEP-2000; 2000US-0232400P.
PR 14-SEP-2000; 2000US-0232401P.
PR 14-SEP-2000; 2000US-0232633P.
PR 14-SEP-2000; 2000US-0232634P.
PR 14-SEP-2000; 2000US-0233065P.
PR 21-SEP-2000; 2000US-0234223P.
PR 21-SEP-2000; 2000US-0234223P.
PR 21-SEP-2000; 2000US-0234274P.
PR 25-SEP-2000; 2000US-0234997P.
PR 25-SEP-2000; 2000US-0234998P.
PR 26-SEP-2000; 2000US-0235484P.
PR 27-SEP-2000; 2000US-0235834P.
PR 27-SEP-2000; 2000US-0235835P.
PR 29-SEP-2000; 2000US-0236327P.
PR 29-SEP-2000; 2000US-0236367P.
PR 29-SEP-2000; 2000US-0236368P.
PR 29-SEP-2000; 2000US-0236369P.
PR 29-SEP-2000; 2000US-0236370P.
PR 02-OCT-2000; 2000US-0236802P.
PR 02-OCT-2000; 2000US-0237037P.
PR 02-OCT-2000; 2000US-0237038P.

XX	PS	Claim 11 SEQ ID NO 801; 980pp; English.
CC	CC	The invention relates to isolated nucleic acid molecules and their encoded secreted proteins. The nucleic acids and proteins are used to prevent, treat or ameliorate a medical condition in e.g. humans, mice, rabbits, goats, horses, cats, dogs, chickens or sheep. They are also used in diagnosing a pathological condition or susceptibility to a pathological condition. Antibodies to the proteins can also be used in alleviating symptoms associated with the disorders and in diagnostic immunoassays e.g. radioimmunoassays or enzyme linked immunosorbent assays (ELISA). Disorders which are diagnosed or treated include autoimmune diseases e.g. rheumatoid arthritis, hyperproliferative disorders e.g. neoplasms of the breast or liver, cardiovascular disorders e.g. cardiac arrest, cerebrovascular disorders e.g. cerebral ischemia, angiodysplasia, nervous system disorders e.g. Alzheimer's disease, infections caused by bacteria, viruses and fungi and ocular disorders e.g. corneal infection, and many other disorders listed in the specification. The polypeptides can also be used to aid wound healing and epithelial cell proliferation, to prevent skin aging due to sunburn, to maintain organs before transplantation, for supporting cell culture of primary tissues, to regenerate tissues and in chemotaxis. The polypeptides can also be used as a food additive or preservative to increase or decrease storage capabilities, fat content, lipid, protein, carbohydrate, vitamins, minerals, cofactors and other nutritional components. The present sequence represents a novel secreted protein of the invention. Note: The sequence data for this patent did not form part of the printed
Query Match	99.7%; Score 1826; DB 4; Length 392;	
Best Local Similarity	99.7%; Pred. No. 5.1e-168;	
Matches 351; Conservative	0; Mismatches 1; Indels 0; Gaps 0;	
OY	1	MESGGRSRLCGFILGTTSTVTALYSVYRKARVSQELKGAKKVHLGEDLKSILSEAPG 60
Dd	41	MESGGRSRLCGFILGTTSTVTALYSVYRKARVSQELKGAKKVHLGEDLKSILSEAPG 100
OY	61	KCPYANITEGANRVSKEITLSNQFENCKGVQLTLDEHKVMWRTHLMNDCSKITHOR 120
Dd	101	KCPVYAITEGANRVSKEITLSNQFENCKGVQLTLDEHKVMWRTHLMNDCSKITHOR 160
OY	121	TNTVPFDLPVEDSDVDVAVRLLKPLDSVDGLGYEVKKPHSPISFTDVIGHYISGERPK 180
Dd	161	TNTVPFDLPVEDSDVDVAVRLLKPLDSVDGLGYEVKKPHSPISFTDVIGHYISGERPK 220
OY	181	GIDTEEMLKVGATLTGVBELVIDNNNSVRLQPPKQMGYYLSSQDFSLLRQRESSVWLW 240
Dd	221	GIDTEEMLKVGATLTGVBELVIDNNNSVRLQPPKQMGYYLSSQDFSLLRQRESSVWLW 280
OY	241	KVALLVGFATCATLFTFLRKQYIQRDERLTKMQSEPFQEHQOLLSRAPREDRESIKS 300
Dd	281	KVALLVGFATCATLFTFLRKQYIQRDERLTKMQSEPFQEHQOLLSRAPREDRESIKS 340
OY	301	ACVVCISFPKSCVFLECGHWCSTECRYALPEPKKCICLRQAIRVIPLYNS 352
Dd	341	ACVVCISFPKSCVFLECGHWCSTECRYALPEPKKCICLRQAIRVIPLYNS 392
RESULT 10		
ID	ABU54917	
AC	ABU54917 standard; protein; 392 AA.	
XX	ABU54917;	
DT	18-MAR-2003 (first entry)	
XX		
DE	Human novel polypeptide #4.	
XX		
KM	Human; neural disorder; immune system disorder; renal disorder; muscular disorder; respiratory disease; reproductive disorder; gastrointestinal disorder; pulmonary disorder; cardiovascular disorder; hyperproliferative disorder; inflammatory disease; allergic reaction; blood related disorder; cancer; immunosuppressive; antiinflammatory; cardiovascular; nephroretropic; cyostatic; antiallergic; thrombolytic; haemostatic; antiflareitrosclerotic.	

XX Homo sapiens.
 OS
 XX US200232753-A1.
 PN
 XX 19-SEP-2002.
 PD
 XX 17-JAN-2001; 2001US-00764864.
 PF
 XX 31-JAN-2000; 2000US-0179065P.
 PR 04-FEB-2000; 2000US-0180628P.
 PR 28-JUN-2000; 2000US-0214886P.
 PR 07-JUL-2000; 2000US-0216647P.
 PR 07-JUL-2000; 2000US-0216880P.
 PR 11-JUL-2000; 2000US-0217487P.
 PR 14-JUL-2000; 2000US-0217496P.
 PR 26-JUL-2000; 2000US-0220963P.
 PR 26-JUL-2000; 2000US-0220964P.
 PR 14-AUG-2000; 2000US-0224518P.
 PR 14-AUG-2000; 2000US-0224519P.
 PR 14-AUG-2000; 2000US-0225267P.
 PR 14-AUG-2000; 2000US-0225268P.
 PR 14-AUG-2000; 2000US-0225270P.
 PR 14-AUG-2000; 2000US-0225447P.
 PR 14-AUG-2000; 2000US-0225757P.
 PR 14-AUG-2000; 2000US-0225758P.
 PR 30-AUG-2000; 2000US-0228686P.
 PR 01-SEP-2000; 2000US-0229287P.
 PR 01-SEP-2000; 2000US-0229343P.
 PR 01-SEP-2000; 2000US-0229344P.
 PR 01-SEP-2000; 2000US-0229345P.
 PR 05-SEP-2000; 2000US-0229509P.
 PR 05-SEP-2000; 2000US-0229513P.
 PR 21-SEP-2000; 2000US-0231413P.
 PR 21-SEP-2000; 2000US-0234223P.
 PR 21-SEP-2000; 2000US-0234274P.
 PR 25-SEP-2000; 2000US-0234997P.
 PR 27-SEP-2000; 2000US-0235834P.
 PR 29-SEP-2000; 2000US-0236377P.
 PR 29-SEP-2000; 2000US-0236378P.
 PR 29-SEP-2000; 2000US-0236379P.
 PR 29-SEP-2000; 2000US-0236380P.
 PR 02-OCT-2000; 2000US-0236382P.
 PR 02-OCT-2000; 2000US-0237037P.
 PR 02-OCT-2000; 2000US-0237038P.
 PR 02-OCT-2000; 2000US-0237039P.
 PR 13-OCT-2000; 2000US-0237040P.
 PR 20-OCT-2000; 2000US-0239935P.
 PR 20-OCT-2000; 2000US-0240960P.
 PR 20-OCT-2000; 2000US-0241785P.
 PR 01-NOV-2000; 2000US-0241809P.
 PR 17-NOV-2000; 2000US-0244617P.
 PR 08-DEC-2000; 2000US-0249299P.
 PR 08-DEC-2000; 2000US-0251866P.
 PR 08-DEC-2000; 2000US-0251868P.
 PR 08-DEC-2000; 2000US-0251869P.
 XX
 XX (ROSEN/) ROSEN C A.
 PA (RUBEN/) RUBEN S M.
 PA (BARA/) BARASH S C.
 XX
 PI Rosen CA, Ruben SM, Barash SC;
 XX
 XX WPI; 2003-147444/14.
 DR N-PSDB; ABX73176.
 XX
 PT New polypeptides and nucleic acids, useful in gene therapy for treating,
 PT inhibiting or preventing e.g. neural, immune system, muscular,
 PT respiratory, reproductive, gastrointestinal, pulmonary, cardiovascular or
 PT renal disorders.

XX Claim 11; SEQ ID NO 801; 402bp; English.
 PS
 CC The invention relates to human novel polypeptides and their associated
 CC polynucleotides. The polypeptides and polynucleotides are useful in gene
 CC therapy for treating, inhibiting or preventing neural disorders, immune
 CC system disorders (e.g. systemic lupus erythematosus, rheumatoid arthritis
 CC and multiple sclerosis), muscular disorders, respiratory diseases (e.g.
 CC nasal vestibulitis, nasal polyps and sinusitis), reproductive disorders,
 CC gastrointestinal disorders, pulmonary disorders, cardiovascular disorders
 CC (e.g. congenital heart defects, Epstein's anomaly and hypoplastic left
 CC heart syndrome), renal disorders (e.g. acute kidney failure and end-stage
 CC renal disease), hyperproliferative disorders (e.g. Hodgkin's disease and
 CC leukaemia), inflammatory diseases (e.g. septic shock, bursitis and
 CC appendicitis), allergic reactions and conditions (e.g. asthma), blood
 CC related disorders (e.g. thrombosis, atherosclerosis and myocardial
 CC infarction) and cancerous diseases. Sequences ABUS54914-ABUS569 and
 CC ABUS5748 represent human novel polypeptides of the invention
 XX
 SQ Sequence 392 AA;
 Query Match 99.7%; Score 1826; DB 6; Length 392;
 Best Local Similarity 99.7%; Pred. No. 5,1e-168;
 Matches 351; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 MESGGRPSLCQFILGTTSVTAALYSYRQARYSOELKAKKHLEBDLKSITSEAPG 60
 DB 41 MESGGRPSLCQFILGTTSVTAALYSYRQARYSOELKAKKHLEBDLKSITSEAPG 100
 QY 61 KCPYAVIAGAVRSYKETLNSQFVENCXGVIQRLTLOEHKVMNNTTHLMDSCXIIHQ 120
 DB 101 KCPYAVIAGAVRSYKETLNSQFVENCXGVIQRLTLOEHKVMNNTTHLMDSCXIIHQ 160
 QY 121 TMTVPEDLVPHEDGVAVRVKPLDSVDLGLFTYKEFHNSIQFTYVIGHYISGERPK 180
 DB 161 TMTVPEDLVPHEDGVAVRVKPLDSVDLGLFTYKEFHNSIQFTYVIGHYISGERPK 220
 QY 181 GIOETEMLKVGATLTGVEGLVDNNSVRLQPKQMGYIYSSQDFSLQROESSVRLW 240
 DB 221 GIOETEMLKVGATLTGVEGLVDNNSVRLQPKQMGYIYSSQDFSLQROESSVRLW 280
 QY 241 KYLALVFGATCATLFTILRQYIQRORRLKQOESEFQHEADQLSRAPEDRESLKS 300
 DB 281 KYLALVFGATCATLFTILRQYIQRORRLKQOESEFQHEADQLSRAPEDRESLKS 340
 QY 301 ACVCLTSFKSCVPLEGCHVCSCTECYRALPEPKKCPICRAITRVPLVNS 352
 DB 341 ACVCLTSFKSCVPLEGCHVCSCTECYRALPEPKKCPICRAITRVPLVNS 392
 RESULT 11
 ABBP1460
 ID ABBP1460 standard; protein, 352 AA.
 AC ABBP1460;
 XX
 DT 30-SEP-2002 (first entry)
 XX
 DE Human NF-KB activating protein SEQ ID NO 73.
 XX
 DE Human; NF-kB; nuclear factor kappa B; mouse; antiinflammatory;
 KW immunomodulator; cytostatic; antiinfective; osteopathic; nootropic;
 KW neuroprotective; anti-HIV; autoimmune disease; cancer; infection;
 KW bone disease; AIDS; neurodegenerative disease; ischaemic disorder.
 XX
 OS Homo sapiens.
 XX
 XX WO200253737-A1.
 XX
 PD 11-JUL-2002.
 XX
 PF 25-DEC-2001; 2001WO-0P011389.

DB 241 KYALVFGFATCATLFFILRKQYLQROERLRLKQMOEFQHEAQLLSRAKPEDRESLKS 300
 QY 301 ACVCLSSFKSCVFLGCGHVCSTCECYRALPEPKKCPICRAITRVPLNYS 352
 DB 301 ACVCLSSFKSCVFLGCGHVCSTCECYRALPEPKKCPICRAITRVPLNYS 352

RESULT 13
 ADU02286
 ID ADU02286 standard; protein; 511 AA.
 XX ADU02286;
 AC ADU02286;
 DT 27-JAN-2005 (first entry)
 DE Novel human polypeptide seqid 753.

KW cytostatic; antipsoriatic; antiinflammatory; gene therapy; Nanodisc;
 KW proliferative disorder; inflammatory disorder; immune disorder;
 KW metabolic disorder; bone disorder; CNS disorder; cancer; psoriasis;
 KW ulcerative colitis; human.

OS Homo sapiens.
 XX MO2004093804-A2.
 EN 04-NOV-2004.
 PD 19-APR-2004; 2004MO-US012047.
 PF 18-APR-2003; 2003US-0463708P.
 PR 18-APR-2003; 2003US-0463732P.
 PR 02-MAY-2003; 2003US-0467199P.
 PR 19-MAY-2003; 2003US-0467230P.
 PR 19-MAY-2003; 2003US-0471306P.
 PR 08-JUL-2003; 2003US-0485223P.
 PR 08-JUL-2003; 2003US-0485224P.
 PR 14-JUL-2003; 2003US-0486464P.
 PR 14-JUL-2003; 2003US-0486480P.
 PR 08-AUG-2003; 2003US-0493573P.
 PR 08-AUG-2003; 2003US-0493577P.
 PR 08-SEP-2003; 2003US-0505059P.

(FIVE-) FIVE PRIME THERAPEUTICS INC.
 PA Lee E, Hestir K, Chu K, Masuoka L, Williams LT;
 PI WPI; 2004-775861/76.
 DR N-PSDB; ADU01554.
 DR New first nucleic acid molecule comprising a polynucleotide sequence
 PT given in the specification, useful in preparing a composition for
 PT diagnosing or treating e.g., cancer, psoriasis or ulcerative colitis.
 XX
 PS Claim 14; SEQ ID NO 753; 291bp; English.

The invention describes a new first nucleic acid molecule comprising a
 CC polynucleotide sequence given in the specification. Also described are:
 CC an animal injected with the nucleic acid molecule; a second nucleic acid
 CC molecule comprising a second polynucleotide sequence that is at least
 CC about 70, 80, 90 or 95% homologous to the first nucleic acid molecule or
 CC that hybridises to the first polynucleotide sequence under high
 CC stringency conditions; a vector comprising the nucleic acid molecule and
 CC a promoter that drives the expression of the nucleic acid molecule; a
 CC host cell transformed; a nucleic acid composition comprising a carrier or
 CC nucleic acid molecule; a nucleic acid composition comprising a carrier or
 CC a buffer and one or more compositions comprising the nucleic acid
 CC molecule, vector or host cell; a substantially purified polypeptide; an
 CC animal injected with the polypeptide; a polypeptide composition
 CC comprising the polypeptide molecule and a carrier or buffer; a cell
 CC culture medium comprising the polypeptide or transfected cells
 CC transfected with the polynucleotide; making a transformed, transfected,

transduced, or infected host cell; synthesising Nanodiscs simultaneously
 CC and for synthesising a series of simultaneously-synthesised Nanodiscs
 CC sequentially utilising a dynamic system; preparing a hydrophobic protein
 CC for determination of crystal structure; immunising a non-human animal;
 CC screening for modulators of hydrophobic protein activity; a diagnostic
 CC kit; determining the presence of the nucleic acid molecule or its
 CC complement; determining the presence of an antibody to the polypeptide in
 CC a sample; an antibody specifically recognising, binding to or modulating
 CC the biological activity of at least one polypeptide encoded by a nucleic
 CC acid molecule or its biologically active fragment; an antibody
 CC composition comprising the antibody and a carrier; a bacteriophage, where
 CC the antibody is displayed on the bacteriophage; a bacterial cell
 CC comprising the bacteriophage; a non-human animal injected with the
 CC antibody composition; a host cell that secretes the antibody; making an
 CC antibody; diagnosing a disease, disorder, syndrome, or condition
 CC comprising cancer, or proliferative, inflammatory, immune, metabolic,
 CC bone, CNS, genetic, bacterial and viral diseases, disorders, syndromes or
 CC conditions in a patient; a modulator composition comprising a modulator
 CC and a carrier; gene therapy; prophylactic or therapeutic treatment of a
 CC subject; an isolated modified cell comprising at least one first
 CC heterologous nucleic acid molecule, where the first heterologous nucleic
 CC acid molecule comprises a first polynucleotide sequence that encodes a
 CC first polypeptide; a non-human animal deficient in the polypeptide or
 CC that over-expresses the polypeptide; isolated tissues derived from the
 CC non-human animal; and one or more cells derived from the non-human
 CC animal. The nucleic acid is useful in preparing a composition for
 CC diagnosing or treating e.g., cancer, psoriasis or ulcerative colitis.
 CC This is the amino acid sequence of a novel human polypeptide of the
 CC invention.

Sequence 511 AA;

Query Match 98.0%; Score 1795; DB 8; Length 511;
 Best Local Similarity 100.0%; Pred. No. 7.6e-165;
 Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MESSGRPSICQPIILGTTSVTAALSYVRQKARYSGLKAKYHAGEDEKSLISEAPG 60
 DB 1 MESSGRPSICQPIILGTTSVTAALSYVRQKARYSGLKAKYHAGEDEKSLISEAPG 60
 QY 61 KCVPAVAVIEGAVRSYKETLNSQFVENCQVYIQLTLQEHKVMWNTTHLAMDCKIIR 120
 DB 61 KCVPAVAVIEGAVRSYKETLNSQFVENCQVYIQLTLQEHKVMWNTTHLAMDCKIIR 120
 QY 121 TMTVPFDIVPHEDGDVAVRLKPLDSYDLGLETYYEKFNHSIGFTDVIHYISGERPK 180
 DB 121 TMTVPFDIVPHEDGDVAVRLKPLDSYDLGLETYYEKFNHSIGFTDVIHYISGERPK 180
 QY 181 GIOETEMLKVGATLTGVELVLDDNNSVRLQPPKQMOYUYSODPDSLQROESSVRLW 240
 DB 181 GIOETEMLKVGATLTGVELVLDDNNSVRLQPPKQMOYUYSODPDSLQROESSVRLW 240
 QY 241 KYALVFGFATCATLFFILRKQYLQROERLRLKQMOEFQHEAQLLSRAKPEDRESLKS 300
 DB 241 KYALVFGFATCATLFFILRKQYLQROERLRLKQMOEFQHEAQLLSRAKPEDRESLKS 300

RESULT 14
 ABJ38698
 ID ABJ38698 standard; protein; 263 AA.
 XX ABJ38698;
 AC ABJ38698;
 DT 04-AUG-2003 (first entry)
 DE Human nucleic acid-associated protein (NAAP) #28.
 KW Human; gene therapy; nucleic acid-associated protein; NAAP;
 KW cell proliferative disorder; cancer; neurological disorder; epilepsy;

KW immune disorder; inflammatory disorder; AIDS; allergy;
 KW developmental disorder; Cushing's syndrome.
 OS Homo sapiens.
 XX WO2003010329-A2.
 XX PD
 XX 06-FEB-2003.
 PF 25-JUL-2002; 2002WO-US023756.
 XX
 XX 26-JUL-2001; 2001US-0308189P.
 PR 27-JUL-2001; 2001US-0308171P.
 PR 02-AUG-2001; 2001US-0310139P.
 PR 03-AUG-2001; 2001US-0309974P.
 PR 08-AUG-2001; 2001US-0311072P.
 PR 10-AUG-2001; 2001US-0311642P.
 PR 10-AUG-2001; 2001US-0311717P.
 PR 12-OCT-2001; 2001US-0329688P.
 XX
 XX (INCYTE GENOMICS INC.
 XX PA
 PI Tang YT, Nguyen DB, Yao MG, Warren BA, Griffin JA, Ison CH;
 PI Forsythe JD, Becha SD, Yue H, Emerling BW, Walla NK, Richardson TW;
 PI Lee EA, Ramakumar J, Elliott VS, He A, Li JX, Hafalia AJA, Yang J;
 PI Santanalla MM, Xu Y, Arvizu CS, Gandhi AR, Borowsky ML, Tran UK;
 PI Burford N, Sprague MW, Baughn MR, Swarnakar A, Policky JL, Lee SY;
 PI Jjiang X, Jackson A, Chang H;
 XX
 XX WPI; 2003-248084/24.
 DR N-PSDB; ABR42547.
 XX
 PT New human nucleic acid associated proteins (NAAP), useful for diagnosing,
 PT treating and preventing diseases or conditions associated with the
 PT aberrant NAAP expression e.g. cancer, AIDS, atherosclerosis, epilepsy, or
 PT infections.
 XX
 XX Claim 1; Page 229; 263pp; English.
 XX
 CC The invention comprises the amino acid and coding sequences of human
 CC nucleic acid-associated proteins (NAAP). The DNA and protein sequences of
 CC the invention are useful for diagnosing, treating and preventing diseases
 CC or conditions associated with the decreased expression or overexpression
 CC of NAAP, such as: cell proliferative disorders (e.g. cancer);
 CC neurological disorders (e.g. epilepsy); immune/inflammatory disorders
 CC (e.g. AIDS and allergies); and developmental disorders (e.g. Cushing's
 CC syndrome). The present amino acid sequence represents a human nucleic
 CC acid-associated protein of the invention
 XX
 XX Sequence 263 AA;
 SQ
 Query Match 72.6%; Score 1328.5; DB 6; Length 263;
 Best Local Similarity 74.7%; Pred. No. 5.4e-120;
 Matches 263; Conservative 0; Mismatches 0; Indels 89; Gaps 1;
 QY 1 MESSGRPSICQILIGTTSVTAALYSVVRKQARVSGELKAKKHLGSDLSLSEARG 60
 DB 1 MESSGRPSICQIFILG----- 16
 QY 61 KCVPAVIEGAVRSVETLNSQFVENCQVIOQLTLOEHKQWNRITTHLMNDSKIIHOR 120
 DB 17 -----TTHLMNDSKIIHOR 31
 QY 121 TTTVPFDLVPHEDGVAVRVLKPLDSVDLGLFTYEKEHPISQSTTVYIGHYISGERPK 180
 DB 32 TTTVPFDLVPHEDGVAVRVLKPLDSVDLGLFTYEKEHPISQSTTVYIGHYISGERPK 91
 QY 181 GJOETHEMLKVGATLTGVELVLDNNNSVRLQPPKQMOYLLSSQPPDSLLQROESSVRM 240
 DB 92 GJOETHEMLKVGATLTGVELVLDNNNSVRLQPPKQMOYLLSSQPPDSLLQROESSVRM 151
 QY 241 KYIALVFGFATCATLFFILRKQYLOREERLRLKOMQEEFOHEHAQLLSRAKPEDRESLKS 300

DB 152 KYIALVFGFATCATLFFILRKQYLOREERLRLKOMQEEFOHEHAQLLSRAKPEDRESLKS 211
 QY 301 ACVCLISFKSCVFLBEGHVCSCTECYRALPEPKKPCICROAIRVILPNS 352
 DB 212 ACVCLISFKSCVFLBEGHVCSCTECYRALPEPKKPCICROAIRVILPNS 263
 RESULT 15
 AAUI6309
 ID AAUI6309 standard; protein, 174 AA.
 XX
 XX AAUI6309;
 AC 07-NOV-2001 (first entry)
 XX
 XX Human novel secreted protein, Seq ID 1262.
 KW Human; immunosuppressive; antiarthritic; antirheumatic; cystostatic;
 KW cardiact; vasotropic; cerebroprotective; nootropic; neuroprotective;
 KW antibacterial; virucide; fungicide; ophthalmological; vulnery;
 KW secreted protein; rheumatoid arthritis; hyperproliferative disorder;
 KW cardiovascular disorder; cardiac arrest; cerebrovascular disorder;
 KW cerebral ischaemia; angio genesis; nervous system disorder;
 KW Alzheimer's disease; infection; ocular disorder; corneal infection;
 KW wound healing; epithelial cell proliferation; skin ageing; food additive;
 KW preservative; antiproliferative.
 XX
 XX Homo sapiens.
 OS
 XX WO200155322-A2.
 XX
 XX 02-AUG-2001.
 PD
 PF 17-JAN-2001; 2001WO-US001341.
 XX
 XX 31-JAN-2000; 2000US-0179065P.
 PR 04-FEB-2000; 2000US-0180628P.
 PR 24-FEB-2000; 2000US-0184664P.
 PR 02-MAR-2000; 2000US-0186350P.
 PR 16-MAR-2000; 2000US-0189874P.
 PR 17-MAR-2000; 2000US-0190076P.
 PR 18-APR-2000; 2000US-0198123P.
 PR 19-MAY-2000; 2000US-0205515P.
 PR 07-JUN-2000; 2000US-0209467P.
 PR 28-JUN-2000; 2000US-0214886P.
 PR 30-JUN-2000; 2000US-0215135P.
 PR 07-JUL-2000; 2000US-0216647P.
 PR 07-JUL-2000; 2000US-0216880P.
 PR 11-JUL-2000; 2000US-0217487P.
 PR 14-JUL-2000; 2000US-0218290P.
 PR 26-JUL-2000; 2000US-0220963P.
 PR 26-JUL-2000; 2000US-0220964P.
 PR 14-AUG-2000; 2000US-0224518P.
 PR 14-AUG-2000; 2000US-0224519P.
 PR 14-AUG-2000; 2000US-0225213P.
 PR 14-AUG-2000; 2000US-0225214P.
 PR 14-AUG-2000; 2000US-0225267P.
 PR 14-AUG-2000; 2000US-0225268P.
 PR 14-AUG-2000; 2000US-0225270P.
 PR 14-AUG-2000; 2000US-0225447P.
 PR 14-AUG-2000; 2000US-0225757P.
 PR 14-AUG-2000; 2000US-0225758P.
 PR 14-AUG-2000; 2000US-0225759P.
 PR 18-AUG-2000; 2000US-0226279P.
 PR 22-AUG-2000; 2000US-0226811P.
 PR 22-AUG-2000; 2000US-0226868P.
 PR 22-AUG-2000; 2000US-0227183P.
 PR 23-AUG-2000; 2000US-0227009P.
 PR 30-AUG-2000; 2000US-0228924P.
 PR 01-SEP-2000; 2000US-0229287P.
 PR 01-SEP-2000; 2000US-0229343P.

PR 01-SEP-2000; 2000US-0229344P.
PR 01-SEP-2000; 2000US-0229345P.
PR 05-SEP-2000; 2000US-0229509P.
PR 05-SEP-2000; 2000US-0229513P.
PR 06-SEP-2000; 2000US-0230437P.
PR 06-SEP-2000; 2000US-0230438P.
PR 08-SEP-2000; 2000US-0231242P.
PR 08-SEP-2000; 2000US-0231243P.
PR 08-SEP-2000; 2000US-0231444P.
PR 08-SEP-2000; 2000US-0231413P.
PR 08-SEP-2000; 2000US-0231414P.
PR 08-SEP-2000; 2000US-0232080P.
PR 08-SEP-2000; 2000US-0232081P.
PR 12-SEP-2000; 2000US-0231968P.
PR 14-SEP-2000; 2000US-0232397P.
PR 14-SEP-2000; 2000US-0232398P.
PR 14-SEP-2000; 2000US-0232399P.
PR 14-SEP-2000; 2000US-0232400P.
PR 14-SEP-2000; 2000US-0232401P.
PR 14-SEP-2000; 2000US-0233063P.
PR 14-SEP-2000; 2000US-0233064P.
PR 14-SEP-2000; 2000US-0233065P.
PR 21-SEP-2000; 2000US-0234223P.
PR 21-SEP-2000; 2000US-0234274P.
PR 25-SEP-2000; 2000US-0234977P.
PR 25-SEP-2000; 2000US-0234988P.
PR 26-SEP-2000; 2000US-0235484P.
PR 27-SEP-2000; 2000US-0235434P.
PR 27-SEP-2000; 2000US-0235836P.
PR 29-SEP-2000; 2000US-0236327P.
PR 29-SEP-2000; 2000US-0236367P.
PR 29-SEP-2000; 2000US-0236368P.
PR 29-SEP-2000; 2000US-0236369P.
PR 29-SEP-2000; 2000US-0236370P.
PR 02-OCT-2000; 2000US-0236802P.
PR 02-OCT-2000; 2000US-0237037P.
PR 02-OCT-2000; 2000US-0237038P.
PR 02-OCT-2000; 2000US-0237039P.
PR 02-OCT-2000; 2000US-0237040P.
PR 13-OCT-2000; 2000US-0239935P.
PR 13-OCT-2000; 2000US-0239937P.
PR 20-OCT-2000; 2000US-0240607P.
PR 20-OCT-2000; 2000US-0241212P.
PR 20-OCT-2000; 2000US-0241785P.
PR 20-OCT-2000; 2000US-0241786P.
PR 20-OCT-2000; 2000US-0241787P.
PR 20-OCT-2000; 2000US-0241808P.
PR 20-OCT-2000; 2000US-0241826P.
PR 01-NOV-2000; 2000US-0244617P.
PR 08-NOV-2000; 2000US-0246474P.
PR 08-NOV-2000; 2000US-0246475P.
PR 08-NOV-2000; 2000US-0246476P.
PR 08-NOV-2000; 2000US-0246477P.
PR 08-NOV-2000; 2000US-0246478P.
PR 08-NOV-2000; 2000US-0246523P.
PR 08-NOV-2000; 2000US-0246524P.
PR 08-NOV-2000; 2000US-0246525P.
PR 08-NOV-2000; 2000US-0246526P.
PR 08-NOV-2000; 2000US-0246527P.
PR 08-NOV-2000; 2000US-0246528P.
PR 08-NOV-2000; 2000US-0246532P.
PR 08-NOV-2000; 2000US-0246609P.
PR 08-NOV-2000; 2000US-0246610P.
PR 08-NOV-2000; 2000US-0246611P.
PR 08-NOV-2000; 2000US-0246613P.
PR 17-NOV-2000; 2000US-0249207P.
PR 17-NOV-2000; 2000US-0249208P.
PR 17-NOV-2000; 2000US-0249209P.
PR 17-NOV-2000; 2000US-0249210P.
PR 17-NOV-2000; 2000US-0249211P.
PR 17-NOV-2000; 2000US-0249212P.
PR 17-NOV-2000; 2000US-0249213P.

PR 17-NOV-2000; 2000US-0249214P.
PR 17-NOV-2000; 2000US-0249215P.
PR 17-NOV-2000; 2000US-0249215P.
PR 17-NOV-2000; 2000US-0249217P.
PR 17-NOV-2000; 2000US-0249218P.
PR 17-NOV-2000; 2000US-0249244P.
PR 17-NOV-2000; 2000US-0249245P.
PR 17-NOV-2000; 2000US-0249264P.
PR 17-NOV-2000; 2000US-0249265P.
PR 17-NOV-2000; 2000US-0249297P.
PR 17-NOV-2000; 2000US-0249299P.
PR 17-NOV-2000; 2000US-0249299P.
PR 17-NOV-2000; 2000US-0249300P.
PR 01-DEC-2000; 2000US-0250160P.
PR 01-DEC-2000; 2000US-0250391P.
PR 05-DEC-2000; 2000US-0251030P.
PR 05-DEC-2000; 2000US-0251988P.
PR 05-DEC-2000; 2000US-0251989P.
PR 06-DEC-2000; 2000US-0256719P.
PR 08-DEC-2000; 2000US-0251479P.
PR 08-DEC-2000; 2000US-0251856P.
PR 08-DEC-2000; 2000US-0251868P.
PR 08-DEC-2000; 2000US-0251869P.
PR 08-DEC-2000; 2000US-0251989P.
PR 08-DEC-2000; 2000US-0251990P.
PR 11-DEC-2000; 2000US-0254097P.
PR 05-JAN-2001; 2001US-0259678P.
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PA (HUMA-) HUMAN GENOME SCI INC.
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PI Rosen CA, Barash SC, Ruben SM;
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XX WPI; 2001-488783/53.
DR N-PSDB; AAS262296.
XX
XX New nucleic acid molecules encoding 461 human secreted proteins for
PT diagnosing, preventing, treating or ameliorating medical conditions and
PT used as food additives or preservatives.
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PS Claim 11; SEQ ID NO 1262; 980pp; English.
XX
CC The invention relates to isolated nucleic acid molecules and their
CC encoded secreted proteins. The nucleic acids and proteins are used to
CC prevent, treat or ameliorate a medical condition in e.g. humans, mice,
CC rabbits, goats, horses, cats, dogs, chickens or sheep. They are also used
CC in diagnosing a pathological condition or susceptibility to a
CC pathological condition. Antibodies to the proteins can also be used in
CC alleviating symptoms associated with the disorders and in diagnostic
CC immunoassays e.g. radioimmunoassays or enzyme linked immunosorbent assays
CC (ELISA). Disorders which are diagnosed or treated include autoimmune
CC diseases e.g. rheumatoid arthritis, hyperproliferative disorders e.g.
CC neoplasms of the breast or liver, cardiovascular disorders e.g. cardiac
CC arrest, cerebrovascular disorders e.g. cerebral ischaemia, angiogenesis,
CC nervous system disorders e.g. Alzheimer's disease, infections caused by
CC bacteria, viruses and fungi and ocular disorders e.g. corneal infection,
CC and many other disorders listed in the specification. The polypeptides
CC can also be used to aid wound healing and epithelial cell proliferation,
CC to prevent skin aging due to sunburn, to maintain organs before
CC transplantation, for supporting cell culture of primary tissues, to
CC regenerate tissues and in chemotaxis. The polypeptides can also be used
CC as a food additive or preservative to increase or decrease storage
CC capabilities, fat content, lipid, protein, carbohydrate, vitamins,
CC minerals, cofactors and other nutritional components. The present
CC sequence represents a novel secreted protein of the invention. Note: The
CC sequence data for this patent did not form part of the printed
Query Match 49.2%; Score 901; DB 4; Length 174;
Best Local Similarity 99.4%; Pred. No. 9, 1e-79;
Matches 173; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 179 PKGIQETEMKLVGATLGVGELVLDNNSVRLQPKQKQVYLSQSDPFSILQROESSVR 238
Db 1 PKGIQETEMKLVGATLGVGELVLDNNSVRLQPKQKQVYLSQSDPFSILQROESSVR 60
QY 239 LMKVLALVFGATCATLFFILRKQYLQROERILRKQMOEFOEHEAQLLSRAKPEDRESL 298

Db	61	LMKVLAIVRGFATCATLFFILRKQYLRQERLRKQMOEFOEHEAQLLSRAKPEDXESL	120
Qy	299	KSACTVCLSSFKSCVFLBEGHVCSTECYRALPEPKCPICROAITRVIPLYN	352
Db	121	KSACTVCLSSFKSCVFLBEGHVCSTECYRALPEPKCPICROAITRVIPLYN	174

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